

```

Db 475 CPTSKKEQPGQEELOPPPR-----TPTTEQLSPPPARPKSAELLQRYSP----- 520
QY 52 TGLFGEDVFRFSAPVYM-----PTWVLRRTTACAGRSVYTEAY-----VTIPV 96
Db 521 -----KKQVRIASPVMOQERRELCPQLPRGSPITLDSQSSPTNAVSGPKKPLPLPI 575
QY 97 GCTCVPEPEKDDADSSINSIDKOGAKLLLGPNDA 130
Db 576 ACR--PRPSNGVNSPNS-----SPGSAP 597

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RESULT 15

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O46545
ID O46545 PRELIMINARY; PRT; 1045 AA.
AC O46545;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 2.
GN CR2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Boroidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE ALPINE;
RA Hein W.R., Dudler L., Marston W., Landsverk T., Young A., Avila D.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038131; AAB92375.1; -.
DR HSP; F10998; LVVD.
DR InterPro; IPR000436; -.
DR Pfam; PF00084; sushi; 14.
DR SMART; SM00032; CCP; 1.
SQ SEQUENCE 1045 AA; 115561 MW; FF58E1A2892C0D59 CRC64;

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Query Match 10.6%; Score 77.5; DB 6; Length 1045;
Best Local Similarity 25.9%; Pred. No. 8.7;
Matches 29; Conservative 13; Mismatches 43; Indels 27; Gaps 5;

QY 15 PPTNLRVSFWAYRISYDPARYLPRYLPEAYLCRGCLTG--LFGEEDVFRFSAPVYMPV 72
Db 423 PPKILNGQKEDRHRVDFPTGSIRY-----SCDPGYVLVGEESIRCTPDGVMIPTA 473
QY 73 VLRRTPACAGRSVYTEAYVTIPVGTCTVPEPEK--ADSINSIDKOGAKL 122
Db 474 PICKAECB-----PVGKQVFKPKNQFIRPDVNSSCD-EGYRL 511

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Search completed: October 5, 2001, 15:23:45
Job time: 190 sec


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RESULT 9
O40633
ID O40633 PRELIMINARY; PRT; 151 AA.
AC O40633;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INTERLEUKIN 17.
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10361;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-488;
RX MEDLINE=98037620; PubMed=9371569;
RA Knaepe A., Hiller C., Thureau M., Wittmann S., Hofmann H.,
RA Fleckenstein B., Fichenscher H.;
RT "The superantigen-homologous viral immediate-early gene iel4/vsag in
RT herpesvirus saimiri-transformed human T cells.";
RL J. Virol. 71:9124-9133(1997).
DR EMBL; Y13183; CAA73627.1; -
SQ SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 107.5; DB 14; Length 151;
Best Local Similarity 31.4%; Pred. No. 0.00063;
Matches 27; Conservative 12; Mismatches 36; Indels 11; Gaps 3;

QY 20 RSVSPWAYRISYDPARYPRYLPEAYCLRGCLTGLFGEEDVFRSAPVYMTVVLRRTPA 79
  ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 65 RSTSPWTLRYNEDQDRYPSVINEAKRYLGCVNA-DGNVDYHMNSVPIQOILVVRK--- 120
  ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 80 CAGGRSVYTYEAY---VTIPVGCTCV 101
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 121 ---GHNPSPNFLEKMLVTVGCTCV 143
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 10
Q19778
ID Q19778 PRELIMINARY; PRT; 148 AA.
AC Q19778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE F25D1.3 PROTEIN.
GN F25D1.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelly P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Green P., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Gresham J., Kirkens T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z73973; CAA98268.1; -
```

```
SQ SEQUENCE 148 AA; 16738 MW; ADB51F438DFB3940 CRC64;

Query Match 13.6%; Score 99; DB 5; Length 148;
Best Local Similarity 29.8%; Pred. No. 0.005;
Matches 28; Conservative 17; Mismatches 35; Indels 14; Gaps 5;

QY 20 RSVSPWAYRISYDPARYPRYLPEAYCLRGCLTGLFGEEDVFRSAPVYMTVVLRRRT 77
  ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 52 RALCPWDSDRVNVQESREPKLIASVCLCRKSRGSGTAF-----CMPIVRKVPILRRV 103
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 78 PAC--AGGRSVYTYEAYVTIPVGCTCVPEPEKDA 108
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 104 -SCDRSTGLWNVYRSTELITVGCCHSVLPRTQRAA 136
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 11
Q9UBG7
ID Q9UBG7 PRELIMINARY; PRT; 520 AA.
AC Q9UBG7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TRANSCRIPTION FACTOR RBP-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RA Koyama K., Isaka S., Okamura S.;
RT "112-pan.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Isaka S., Koyama K., Nakamura Y., Okamura S., Azuma C., Kimura T.;
RT "Human RBP-L.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB024964; BAA88232.1; -
DR EMBL; AB026048; BAA86121.1; -
DR InterPro; IPR002909; -
DR Pfam; PF01833; TIG; 1.
SQ SEQUENCE 520 AA; 57038 MW; BACF92459A77ACFB CRC64;

Query Match 10.9%; Score 79.5; DB 4; Length 520;
Best Local Similarity 28.3%; Pred. No. 2.4;
Matches 28; Conservative 12; Mismatches 36; Indels 23; Gaps 4;

QY 27 YRISYDPARYPRYLPEAYCLRGCLTGLFGEEDVFRSAPVYMTVVLRRTPACAGG--- 83
  ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 426 YRYGVEPAVLVCVVDVAFC-----SDRWLRAPITIPMSLVR-----ADGLEF 470
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 84 ----RSVYTYEAYVTIPVGCTCVPEPEKDAINSIDKQ 118
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 471 PSAFSTYTPYTSVRP-GHPGVPEPATDADALLESIHQ 508
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 12
Q9XUH9
ID Q9XUH9 PRELIMINARY; PRT; 226 AA.
AC Q9XUH9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ZK39.8 PROTEIN.
GN ZK39.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
```


DT	01-MAR-2001 (TtEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TtEMBLrel. 16, Last annotation update)
OS	CYTOKINE CX2 PRECURSOR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]
RN	NCHI_TaxID=9606;
RN	SEQUENCE FROM N.A.
RA	Zhang W., He L., Wan T., Yuan Z., Cao X.;
RA	"Novel human cytokine CX2 with homology to IL-17.";
RT	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF142410; AAG27921.1; -.
SQ	SEQUENCE 197 AA; 21784 MW; BAFB49F631A7A768 CRC64;
Query Match	25.7%; Score 187.5; DB 4; Length 197;
Best Local Similarity	40.2%; Pred. No. 2.4e-12;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;	
QY	17 TNLRVSPWARYISYPARYPRYLPEAYLCRCGLTGLFGEDVFRRFSAPVMPTVLVLR 76 : : : : :
Db	101 THQRSIPWRYRVTDDEDPVKLAFLACILCRGCI DARTGRETAALNSVRLLQSLLVLR 160 : : : : :
QY	77 TPACAGRSVYTEA-----YVTIPVGCTCV 101 : : : : : :
Db	161 RPSRDGSLPTPGAFATFTFIHVPVGCTCV 192 : : : : : :
RESULT 3	
ID Q9EQ16	PRELIMINARY; PRT; 178 AA.
ID AC Q9EQ16;	
DT 01-MAR-2001 (TtEMBLrel. 16, Created)	
DT 01-MAR-2001 (TtEMBLrel. 16, Last sequence update)	
DT 01-MAR-2001 (TtEMBLrel. 16, Last annotation update)	
DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).	
OS Mesocricetus auratus (Golden hamster).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
OC Mesocricetus.	
OX NCHI_TaxID=10036;	
RN [1]	
RN	SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,	
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;	
RT "Identification of a novel IL-17 related factor: Demonstration of	
RT neuronal expression and evaluation as a candidate for the chromosome	
RT 5q-linked form of Charcot-Marie-Tooth disease."	
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.	
DR EMBL; AF218725; AAG44134.1; -.	
FT NON_TER 178	
SQ SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;	
Query Match	24.2%; Score 176.5; DB 11; Length 178;
Best Local Similarity	42.0%; Pred. No. 3.2e-11;
Matches 42; Conservative 9; Mismatches 42; Indels 7; Gaps 2;	
QY	8 PADRRFRPP-----TNLRVSPWAYRISYPARYPRYLPEAYLCRCGLTGLFGEDVRF 62 : : : :
Db	79 PAKRRCEVNQLWLNSKRSLPWSYGNHDFSRTPADLPPEARCLCGVCNPFTMQEGRSM 138 : : : :
QY	63 RSAPVYPTVLVLR--TPACAGRSVVTEAVVTIPVGCTC 100 : :
Db	139 VSVPFVSQPVRRKLCPPPPRPGRHVVMETIAVGCTC 178 : :
RESULT 4	
ID Q9UHF5	PRELIMINARY; PRT; 180 AA.
ID AC Q9UHF5;	
DT 01-MAY-2000 (TtEMBLrel. 13, Created)	

DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)	
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)	
DE	CYTOKINE-LIKE PROTEIN ZCYT07 (INTERLEUKIN 20) (INTERLEUKIN 17B)	
DE	(NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).	
GN	ZCYT07 OR IL20.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
EN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,	
RA	Martinez T., Hoffman R., O'Hara P.;	
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	
EN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20317118; PubMed=10749887;	
RA	Shi Y., Ullrich S.-J., Zhang J., Connolly K., Grzegorzewski K.J.,	
RA	Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,	
RA	Ruben S.M., Knayzev I., Cho Y.H., Kao V., Wilkinson K.A.,	
RA	Carrell J.A., Ebner R.;	
RT	"A novel cytokine receptor-ligand pair. Identification, molecular	
RT	characterization, and in vivo immunomodulatory activity.";	
RL	J. Biol. Chem. 275:19167-19176(2000).	
EN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20105548; PubMed=10639155;	
RA	Li H., Chen J., Huang A., Stinson J., Heidens S., Foster J., Dowd P.,	
RA	Gurney A.L., Wood W.I.;	
RT	"Cloning and Characterization of IL-17B and IL17C, Two New Members of	
RT	the IL-17 Cytokine Family.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).	
EN	[4]	
RP	SEQUENCE FROM N.A.	
RA	Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,	
RA	Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;	
RT	"Identification of a novel IL-17 related factor: Demonstration of	
RT	neural expression and evaluation as a candidate for the chromosome	
RT	5q-linked form of Charcot-Marie-Tooth disease.";	
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
EN	[5]	
RP	SEQUENCE FROM N.A.	
RX	Zhang W., Wang J., Cao X.;	
RT	"Novel cytokine homology with interleukin-17.";	
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF184969; AAF01318.1;	
DR	EMBL: AF212311; AAF78775.1;	
DR	EMBL: AF152098; AAF28104.1;	
DR	EMBL: AF218727; AAG44136.1;	
DR	EMBL: AF110385; AAG39637.1;	
SQ	SEQUENCE 180 AA; 20437 MW; F1B0BC1446D0B14A CRC64;	
Query Match 23.9%; Score 174; DB 4; Length 180;		
Best Local Similarity 43.7%; Pred.No. 6e-11;		
Matches 38; Conservative 9; Mismatches 38; Indels 2; Gaps		
QY	17 TNLRSVSPWARYISYDARYPRYLPEAYCLRCGLCTGLFGEEDVFRSAPVYMTVVLRR 76	
Db	93 SNKRLSPWGYSINHDPRIPLVDLPPEARCLCLGCNVNFTMQEDRSWVSVPVFSQVPRRR 152	
QY	77 --TPACAGGRSVTEAYVTIPVGCTCV 101	
Db	153 LCPPPPRTGCRQAVMETIAGVCTCI 179	
RESULT 5		
Q9QXT6		
ID	Q9QXT6 PRELIMINARY; PRT; 180 AA.	
AC	Q9QXT6	
DT	01-MAY-2000 (Tremblrel. 13, Created)	
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)	
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)	

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	187.5	25.7	197	4	Q9P0M4		Q9P0M4 homo sapien
2	187.5	25.7	197	4	Q9HC75		Q9HC75 homo sapien
3	176.5	24.2	178	11	Q9EQ16		Q9eq16 mesocricetus
4	174	23.9	180	4	Q9OHF5		Q9uhf5 homo sapien
5	173	23.7	180	11	Q9QXT6		Q9qxt6 mus musculus
6	151	20.7	111	11	Q9EQ17		Q9eq17 rattus norv
7	119.5	16.4	78	4	Q9NUE6		Q9nue6 homo sapien
8	110.5	15.2	177	4	Q9H293		Q9h293 homo sapien
9	107.5	14.7	151	14	Q4O633		Q4O633 salmirlaine
10	99	13.6	148	5	Q19778		Q19778 caenorhabdi
11	79.5	10.9	520	4	Q9UBG7		Q9ubg7 homo sapien
12	78.5	10.8	226	5	Q9XUH9		Q9xuh9 caenorhabdi
13	78	10.7	552	4	Q95723		Q95723 homo sapien
14	78	10.7	805	5	Q9VFD4		Q9vfd4 drosophila
15	77.5	10.6	1045	6	Q46545		Q46545 ovis aries
16	76	10.4	242	2	Q9PL24		Q9pl24 chlamydia m
17	75.5	10.4	509	10	Q48780		Q48780 arabidopsis
18	75	10.3	178	2	Q9X0U1		Q9x0u1 thermotoga
19	75	10.3	242	2	Q84019		Q84019 chlamydia t

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Db 282 YASGTSILGGSDSPVFEGVGGPPPPAAP 311

RESULT 15

RPB1_DROME STANDARD; PRT; 1896 AA.

AC P04052;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6).

GN RPII215.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

FN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89218930; PubMed=2496296;

RA Jockerst R.S., Weeks J.R., Zehring W.A., Greenleaf A.L.;

RT "Analysis of the gene encoding the largest subunit of RNA polymerase II in Drosophila.";

RT Mol. Gen. Genet. 215:266-275(1989).

RN [2]

RP SEQUENCE OF 1-472 FROM N.A.

RX MEDLINE=85282618; PubMed=2992806;

RA Biggs J., Seearles L.L., Greenleaf A.L.;

RT "Structure of the eukaryotic transcription apparatus: features of the gene for the largest subunit of Drosophila RNA polymerase II.";

RT Cell 42:611-621(1985).

RN [3]

RP SEQUENCE OF 1441-1889 FROM N.A.

RX MEDLINE=88094402; PubMed=3122024;

RA Allison L.A., Wong J.K.-C., Fitzpatrick V.D., Moyle M., Ingles C.J.;

RT "The C-terminal domain of the largest subunit of RNA polymerase II of Saccharomyces cerevisiae, Drosophila melanogaster, and mammals: a conserved structure with an essential function.";

RT Mol. Cell. Biol. 8:321-329(1988).

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + RNA(N).

CC -1- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM TEN TO TWELVE DIFFERENT POLYPEPTIDES. THE 215 KDA POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED. THE PHOSPHORYLATION ACTIVATES POL2.

CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II' FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S AND TRNA GENES.

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

CC

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CC -----

CC EMBL; M27431; AAA28868.1; -

CC EMBL; M11798; AAA28863.1; -

CC EMBL; M19537; AAA28827.1; -

CC PIR; S04457; RNPF2L.

CC FlyBase; FBgn0003277; RpiI215.

CC InterPro; IPR000684; -

CC InterPro; IPR000722; -

CC InterPro; IPR002879; -

CC

```

Db      24  ACCLDGPPPIVPHRRRRRIIAALRSVLNRWDTTPRARSQDQVTSHAVLLIGHNRPVRRHGG  83
Qy      39  YLPEAYCLRCGC-----LTGLFGEEDVR-----FRSAPVMTPTVVLRRTPACAGG-----  83
Db      84  ELPRGALALACIALLMGIIVGCTVTVDGTAMPDPTNVPAPRVSSVSASVSAATSSIRE  14
Qy      84  ----RSVYTEAYVPIPVGCTCVPEPKDA-DSINSSIDKQAKILLGENDAPA  131
Db     144  SROQSLSITTKA---IRTSCDALAAATSKDAIDKVNAYVAAFNOGRNTGTGTEGPA  193

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RESULT	14
TTP_BOVIN	
ID	TTP_BOVIN
AC	P53781
STANDARD;	PRT;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	TRISTETRAPOLINE (TTP) (TIS11A PROTEIN) (TIS11) (2FP-36) .
GN	2FP36.

mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
PC TISSUE=Liver;
RP MEDLINE=96027638; Pubmed=7559666;
EX Lai W.S., Thompson M.J., Taylor G.A., Liu Y., Blackshear P.J.;
RA "Promoter analysis of zfp-36, the mitogen-inducible gene encoding the
RT zinc finger protein tristetraprolin.";
RL J. Biol. Chem. 270:25266-25272(1995).
CC -1- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
CC STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
CC HAS BEEN EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.
CC
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
CC -1- SIMILARITY: CONTAINS 2 CX(8)CX(5)CX(3)H-TYPE ZINC FINGERS.
CC
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CC or send an email to license@isb-sib.ch).

	Nuclear protein; Repeat;	Metal-binding; Zinc-finger; DNA-binding.
KW	69	73
FT	REPEAT	P-P-P-P-G.
FT	REPEAT	P-P-P-P-G.
FT	REPEAT	P-P-P-P-G.
FT	ZN_FING	CX(8)CX(5)CX(3)H-TYPE.
FT	ZN_FING	CX(8)CX(5)CX(3)H-TYPE.
FT	ZN_FING	145 164
Q3	SEQUENCE	324 AA; 34087 MW; 6046057E9EA378EE CRC64;

QY	60	VRFSPVYMPYTVLRR	---TPACAGGRSVYTEAYTV	IPVGCCTVPEPEK	DADSI	SSIDK	11
DB	231	---FSAAPHGL	----CRRDPTFACPCSR	RATPNSV	GWPGVGLA	---	RSFSAHSLGSDPDE
QY	118	---QQAQL	-----LLGPNDA	PAGP	133		

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION
 DE ASSOCIATED PROTEIN 6) (MDA-6) (p21) (CDK-INTERACTING PROTEIN 1).
 GN CDKN1A OR CDKN1 OR CIP1 OR WAF1 OR MDA6 OR SD11 OR P1C1 OR CAP20.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=94061996; PubMed=8242751;
 RX Harper J.W., Adami G.R., Wei N., Keyomarsi K., Ellledge S.J.;
 RA "The p21 Cdk-Interacting Protein Cip1 is a potent inhibitor of G1
 RT cyclin-dependent kinases.";
 RL Cell 75:805-816(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94061997; PubMed=8242752;
 RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
 RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
 RT "WAF1, a potential mediator of p53 tumor suppression.";
 RL Cell 75:817-825(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94081955; PubMed=8259214;
 RA Xiong Y., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;
 RT "p21 is a universal inhibitor of cyclin kinases.";
 RL Nature 366:701-704(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Fisher P.B.;
 RT "Use of a sensitive and efficient subtraction hybridization protocol
 RT for the identification of genes differentially regulated during the
 RT induction of differentiation in human melanoma cells.";
 RL Mol. Cell. Differ. 1:285-299(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Lin J., Herlyn M., Kerbel R.S., Weissman B.E.,
 RA Welch D.R., Fisher P.B.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94170884; PubMed=8125163;
 RA Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.;
 RT "Cloning of senescent cell-derived inhibitors of DNA synthesis using
 RT an expression screen.";
 RL Exp. Cell Res. 211:90-98(1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95384154; PubMed=7655464;
 RA Mouses S., Oezcelik H., Lee P.D., Malkin D., Bull S.B.,
 RA Andrusis I.L.;
 RT "Two variants of the CIP1/WAF1 gene occur together and are associated
 RT with human cancer.";
 RL Hum. Mol. Genet. 4:1089-1092(1995).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Palmer S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-160.
 RX MEDLINE=97015085; PubMed=8861913;
 RA Gulbis J.M., Keinan Z., Hurwitz J., O'Donnell M., Kuriyan J.;
 RT "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with
 RT human PCNA.";
 RL Cell 87:297-306(1996).
 CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
 CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES,
 CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.
 CC -1- INDUCTION: BY THE P53 TUMOR SUPPRESSOR/ONCOGENE. ALSO BY MEZEREIN
 CC (ANTILEUKEMIC COMPOUND) AND BY IFN-BETA.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
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 CC
 CC EMBL; L25610; AAA16109.1; -
 CC EMBL; S67388; AAB29246.1; -
 CC EMBL; U09579; AAB85641.1; -
 CC EMBL; U03106; AAC04313.1; -
 CC EMBL; L26165; AAA19811.1; -
 CC EMBL; L47233; AAB59560.1; ALT_INIT.
 CC EMBL; Z85996; CAB06656.1; -
 CC PIR; S39357; S39357.
 CC SWISS-2DPAGE; P38936; HUMAN.
 CC MIM; 116899; -
 KW Cell cycle; Nuclear protein; Zinc-finger.
 FT ZN_FING 13 41 C4-TYPE (POTENTIAL).
 FT DOMAIN 141 156 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 164 AA; 18119 MW; 98D1E7C519ADFCA9 CRC64;

Query Match 9.8%; Score 71.5; DB 1; Length 164;
 Best Local Similarity 25.2%; Pred. No. 1.1;
 Matches 39; Conservative 10; Mismatches 53; Indels 53; Gaps 6;
 QY 3 PAG-----GRPADRRRPPTNLRVSVPWAYRISYDPARYPRYLPEAYCLCRG----- 50
 DB 4 PAGDVQRNFCGSKACRRLFGPVDSEQLS-----RDCDALMAGCLOEAR 46
 QY 51 -----ITGLFGEDVFRFSAP-VYMTVVVLRTPACAGGRSVYT----- 88
 DB 47 ERWNFDFVTETPLEGDFAWERVRLGLPKLYLPTGPRGRDELGGRRRPTSPALLOGTA 106
 QY 89 -EAYVTIPGCTCVPEPEKDAD-SINSSIDKQKAK 121
 DB 107 EEDHVDLSLCTLVPRSGEQAGSGPGGDSQGRK 141
 RESULT 12
 Y450_HUMAN
 ID Y450_HUMAN STANDARD; PRT; 425 AA.
 AC 075038;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN KIAA0450.
 GN KIAA0450
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98116662; PubMed=9455484;
 RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
 RA Nakajima D., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones in size-fractionated cDNA libraries
 RT from human brain.";
 RL DNA Res. 4:345-349(1997).
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KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
 KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 18
 FT CHAIN 19 358 ALPHA-FACTOR XIIA HEAVY CHAIN.
 FT CHAIN 359 603 ALPHA-FACTOR XIIA LIGHT CHAIN.
 FT CHAIN 359 603 FIBRONECTIN TYPE-II.
 FT DOMAIN 46 87 EGF-LIKE 1.
 FT DOMAIN 93 130 FIBRONECTIN TYPE-I.
 FT DOMAIN 132 172 EGF-LIKE 2.
 FT DOMAIN 173 209 KRINGLE.
 FT DOMAIN 216 294 PRO-RICH.
 FT DOMAIN 312 342 CATALYTIC.
 FT DOMAIN 359 603 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 398 398 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 447 447 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 551 551 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 97 109 BY SIMILARITY.
 FT DISULFID 103 118 BY SIMILARITY.
 FT DISULFID 120 129 BY SIMILARITY.
 FT DISULFID 134 162 BY SIMILARITY.
 FT DISULFID 160 169 BY SIMILARITY.
 FT DISULFID 172 188 BY SIMILARITY.
 FT DISULFID 182 197 BY SIMILARITY.
 FT DISULFID 199 208 BY SIMILARITY.
 FT DISULFID 216 294 BY SIMILARITY.
 FT DISULFID 237 276 BY SIMILARITY.
 FT DISULFID 265 289 BY SIMILARITY.
 FT DISULFID 345 472 BY SIMILARITY.
 FT DISULFID 383 399 BY SIMILARITY.
 FT DISULFID 391 461 BY SIMILARITY.
 FT DISULFID 422 425 BY SIMILARITY.
 FT DISULFID 488 557 BY SIMILARITY.
 FT DISULFID 520 536 BY SIMILARITY.
 FT DISULFID 547 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 603 AA; 66795 MW; 48DC6B946FB9ED59 CRC64;

Query Match 10.3%; Score 75; DB 1; Length 603;
 Best Local Similarity 22.2%; Pred. No. 2.1;
 Matches 37; Conservative 17; Mismatches 59; Indels 54; Gaps 7;

QY 2 CPAGGRPADRRPRPT-NLRVSPWAYRISVDPARYPRV-----LPEAY 44
 DB 60 CLHKGRGPRWCATPNPDQDQWYCL--EPKKVKDCSKHNPQRGGICVNTLSSPH 117
 QY 45 CLRCGLTG-----LFGEEDVFRFSAPV-----YMPVTVL 74
 DB 118 CLCPDLTKGKHCOREKCFEPQLHRFFHENEIWFRTGPAGVAKCHCKGPDHCKQMHSQEC 177
 QY 75 RTRPACAGRSVYTRAY--VTIPVGCTCTVPEPEKDAADSIINSIDKQG 119
 DB 178 QTNPCNLNGRCLEVEGHILDCPMGT---GPFCDLDTTASCYEGRG 221

RESULT 8
 YAR2_SCHPO STANDARD; PRT; 1273 AA.
 AC Q10135;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HYPOTHETICAL 142.5 KDA PROTEIN C23E2.02 IN CHROMOSOME I.
 GN SPAC23E2.02.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=972;
 RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: Z68887; CAA93114.1; .
 DR InterPro: IPR002937; .
 DR Pfam: PF01593; Amino_oxidase; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 1028 1048 POTENTIAL.
 SQ SEQUENCE 1273 AA; 142489 MW; 3FEFF6433DF3C0B6 CRC64;

Query Match 10.2%; Score 74.5; DB 1; Length 1273;
 Best Local Similarity 25.6%; Pred. No. 5.4;
 Matches 22; Conservative 15; Mismatches 48; Indels 1; Gaps 1;

QY 46 LCRGCLTGLFGEEDVFRFSAPVYMTVVLRTTPACAGRSVYTRAYTIPVGCTCTVPEPE 105
 DB 520 ICARQLTGLFSQYSSFLSKNELPKVILEAKERTGGR-IYSRALPVSHTSATQINHT 578
 QY 106 KDASINSSIDKQAKLLGPNDA 131
 DB 579 SNSNSISNSTSLNPKDVTDP Ships 604

RESULT 9
 CR2_HUMAN STANDARD; PRT; 1033 AA.
 ID CR2_HUMAN AC P20023;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)
 DE (EPSTEIN-BARR VIRUS RECEPTOR) (EBV RECEPTOR) (CD21 ANTIGEN).
 GN CR2 OR C3DR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89123277; PubMed=2563370;
 RA Fujisaku A., Harley J.B., Frank M.B., Gruner B.A., Frazier B.,
 RA Holers V.M.;
 RT "Genomic organization and polymorphisms of the human C3d/Epstein-Barr
 RT virus receptor.";
 RL J. Biol. Chem. 264:2118-2125(1989).
 RN [2]
 RP SEQUENCE OF 226-233; 256-267; 332-341; 667-677 AND 898-908.
 RX MEDLINE=86287311; PubMed=3016712;
 RA Weis J.J., Fearon D.T., Klickstein L.B., Wong W.W., Richards S.A.,
 RA de Bruyn Kops A., Smith J.A., Weis J.H.;
 RT "Identification of a partial cDNA clone for the C3d/Epstein-Barr
 RT virus receptor of human B lymphocytes: homology with the receptor for
 RT fragments C3b and C4b of the third and fourth components of
 RT complement.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).
 RN [3]
 RP SEQUENCE OF 492-556 FROM N.A. (SHORT ISOFORM).
 RX MEDLINE=93294286; PubMed=8390533;
 RA Sinha S.K., Todd S.C., Hedrick J.A., Speiser C.L., Lambiris J.D.,
 RA Tsoukas C.D.;
 RT "Characterization of the EBV/C3d receptor on the human Jurkat T cell
 RT line: evidence for a novel transcript.";
 RL J. Immunol. 150:5311-5320(1993).

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:20:15 ; Search time 11.55 Seconds
(without alignments)
394.457 Million cell updates/sec

Title: US-09-320-713-4_COPY_28_160

Perfect score: 729

Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLLPNDAPAGP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130.5	17.9	155	1 IL17_HUMAN	Q16552 homo sapien
2	113.5	15.6	158	1 IL17_MOUSE	Q62386 mus musculu
3	108.5	14.9	151	1 VG13_HSVSA	P24916 herpesvirus
4	108	14.8	150	1 IL17_RAT	O61453 rattus norv
5	75.5	10.4	610	1 THIC_RHET	O34291 rhicobulum e
6	75	10.3	362	1 A2HS_PIG	P29700 sus scrofa
7	75	10.3	603	1 FA12_CAVPO	Q04962 cavia porce
8	74.5	10.2	1273	1 YAR2_SCHPO	Q10135 schizosacch
9	73.5	10.1	1033	1 CR2_HUMAN	P20023 homo sapien
10	73	10.0	3358	1 PGCY_MOUSE	O62059 mus musculu
11	71.5	9.8	164	1 CDN1_HUMAN	P38936 homo sapien
12	71.5	9.8	425	1 Y450_HUMAN	O75038 homo sapien
13	70.5	9.7	265	1 YM40_MYCTU	Q10522 mycobacteri
14	69.5	9.5	324	1 TTP_BOVIN	P53781 bos taurus
15	69.5	9.5	1896	1 RP11_DROME	P04052 drosophila
16	68.5	9.4	191	1 MOBA_RHOCA	O9x7k0 rhodobacter
17	68.5	9.4	342	1 HXCA_MOUSE	P31257 mus musculu
18	68.5	9.4	1075	1 NFC3_MOUSE	P97305 mus musculu
19	67.5	9.3	298	1 MYOD_CHICK	P16075 gallus gall
20	67.5	9.3	384	1 DUS9_HUMAN	O99956 homo sapien
21	67	9.2	2273	1 HFAL_YEAST	P28874 saccharomyc
22	66.5	9.1	1117	1 TCF8_MOUSE	O64318 mus musculu
23	66	9.1	676	1 DNLJ_THETH	P26996 thermus aqu
24	65.5	9.0	170	1 PLGE_HUMAN	P49763 homo sapien
25	65.5	9.0	500	1 STCL_EMENI	Q00707 emericehia
26	65	8.9	345	1 YJUN_ECOLI	P39400 escherichia
27	65	8.9	376	1 METK_AQUAE	O67222 aquifex aeo
28	65	8.9	802	1 ACSB_ACEXY	P37716 acetobacter
29	64.5	8.8	285	1 HXA4_MOUSE	P06798 mus musculu
30	64.5	8.8	342	1 HXCA_HUMAN	O9nyd6 homo sapien
31	64.5	8.8	374	1 RLIG_BPT4	P00971 bacteriophag
32	64	8.8	277	1 HXDB_NOTVI	P31263 notophthalm
33	64	8.8	286	1 PYR1_SYNEL	P50034 synechococc

34	64	8.8	497	1 CPDH_MACFA	Q29488 macaca fasc
35	64	8.8	3396	1 PGCY_HUMAN	P13611 homo sapien
36	63.5	8.7	419	1 IRE3_MOUSE	P70671 mus musculu
37	63.5	8.7	429	1 ELK1_MOUSE	P41969 mus musculu
38	63.5	8.7	521	1 DRTS_TRYCR	Q27793 trypanosoma
39	63.5	8.7	649	1 KPCI_APLCA	Q16974 aplysia cal
40	63.5	8.7	1170	1 DP3A_TREPA	O83675 treponema p
41	63	8.6	347	1 FOS_CYPCA	P79702 cyprinus ca
42	62.5	8.6	153	1 NEUV_FUGRU	O42499 fugu rubrip
43	62.5	8.6	262	1 MI43_MYCIT	Q03490 mycobacteri
44	62.5	8.6	322	1 SUCA_CABEL	P53596 caenorhabdi
45	62.5	8.6	329	1 TAL_MOUSE	P22091 mus musculu

ALIGNMENTS

RESULT	1
IL17_HUMAN	
ID	IL17_HUMAN
AC	Q16552;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	INTERLEUKIN-17 PRECURSOR (IL-17) (CYTOTOXIC T LYMPHOCYTE-ASSOCIATED
DE	ANTIGEN 8) (CTLA-8).
GN	IL17 OR CTLA8.
OS	Homo sapiens (Human).
OC	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96281911; PubMed=8676080;
RA	Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Ait-Yahia S.,
RA	Maat C., Pin J.-J., Garrone P., Garcia E., Saeland S., Blanchard D.,
RA	Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Blanchereau J.,
RA	Lebecque S.;
RT	"T cell interleukin-17 induces stromal cells to produce
RT	proinflammatory and hematopoietic cytokines.";
J.	J. Exp. Med. 183:2593-2603(1996).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	TISSUE=T-cell;
RC	MEDLINE=96094436; PubMed=7499828;
RX	Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,
RA	Spriggs M.K., Armitage R.J.;
RT	"Human IL-17: a novel cytokine derived from T cells.";
RT	J. Immunol. 155:5483-5486(1995).
CC	-I- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
CC	HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE
CC	INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.
CC	-I- SUBUNIT: HOMODIMER.
CC	-I- SUBCELLULAR LOCATION: SECRETED.
CC	-I- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.
CC	-I- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.
CC	-I- SIMILARITY: STRONG, TO OTHER MAMMALIAN INTERLEUKIN-17 AND TO
CC	HERPESVIRUS SAIMIRI IMMEDIATE EARLY GENE 13 PROTEIN.
CC	-----
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CC	-----
DR	EMBL; Z58820; CAA91233.1; -
DR	EMBL; U32659; AAC50341.1; -
DR	MIM; 603149; -
KW	Cytokine; Glycoprotein; T-cell; Antigen; Signal.
FT	SIGNAL 1 23 POTENTIAL.
FT	CHAIN 24 155 INTERLEUKIN-17.


```

versican precursor - mouse
N:Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan versican
N:Contains: glial hyaluronate-binding protein
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55535
R:Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A:Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated from embryonic mouse brain
A:Reference number: A55535; MUID:95122551
A:Accession: A55535
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-2397 <RES>
A:Cross-references: GB:D16263; NID:g962460; PIDN:BAA03796.1; PID:g962461
C:Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EGF homology
F:1-20/Domain: signal sequence <status predicted> <SIG>
F:21-1654/Domain: versican <status predicted> <NAT>
F:167-244/Domain: link protein repeat homology <LNK1>
F:265-346/Domain: link protein repeat homology <LNK2>
F:2095-2126/Domain: EGF homology <EG1>
F:2133-2164/Domain: EGF homology <EG2>
F:2171-2291/Domain: C-type lectin homology <LCH>
F:2298-2354/Domain: complement factor H repeat homology <FHD>

```

Query Match 10.0%; Score 73; DB 1; Length 2397;
Best Local Similarity 32.1%; Pred. No. 42;
Matches 26; Conservative 10; Mismatches 33; Indels 12; Gaps 4;

Qy	54	LFGEDVFRSAPYMPVVLRRTACAGRSVY-TE-AVYTIPVGCTCP-----EPEK 106
Db	2074	LIGISEESVEGTAVYLPGLDCKNPNCLNGTCYPTETSVY-----CTCAPGYSGDOEL 2128

QY 107 DADSINSSIDKQGAKLLGPN 127

Pb 2129 DEDECHSNPCRNGATCVDGFN 2149

RESULT	15
--------	----

168674
Cyclin-dependent kinase - human (fragment)
N:Alternate names: probable DNA synthesis inhibitor
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 01-Dec-2000
C:Accession: 168674; A49437; I53412; S39357
R:Mousses, S.; Ozcelik, H.; Lee, P.D.; Malkin, D.; Bull, S.B.; Andrulis, I.L.
Hum. Mol. Genet. 4, 1089-1092, 1995
A:Title: Two variants of the Cipl1/WAF1 gene occur together and are associated with human
A:Reference number: I54380; MUID:95384154
A:Accession: 168674
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-181 <RES>
A:Cross-references: GB:I47233; NID:g986878; PIDN:AA859560.1; PID:g986879
R:Harper, J.W.; Adam, G.R.; Wei, N.; Keyomarsi, K.; Elledge, S.J.
Cell 75, 805-816, 1993
A:Title: The p21 Cdk-interacting protein Cipl1 is a potent inhibitor of G1 cyclin-dependent
A:Reference number: A49437; MUID:94061996
A:Accession: A49437
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 18-181 <RE3>
A:Cross-references: GB:I25610; NID:g425142; PIDN:AAA16109.1; PID:g425143
R:Noda, A.; Ning, Y.; Venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.
Exp. Cell Res. 211, 90-98, 1994
A:Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expression
A:Reference number: I53412; MUID:94170884
A:Accession: I53412
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 18-181 <RE2>

A71568
hypothetical protein CT016 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: A71568
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: A71568
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-242 <ARN>
A:Cross-references: GB:AE001276; GB:AE001273; NID:g3328399; PIDN:AAC67606.1; PID:g3328400
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT016

Query Match 10.3%; Score 75; DB 2; Length 242;
Best Local Similarity 25.0%; Pred. No. 2.1;
Matches 20; Conservative 7; Mismatches 21; Indels 32; Gaps 3;
QY 41 PEAYCLRCGLTGL-----FGEDVFRSAPVYMTVVLRRTPACAGRSVYT--- 88
DB 161 PEPHCNCLHCQIGRATVEEDAGVSDLTFRSWDI-----SOSGEKMYTVD 208
QY 89 -----EAYVTIPVGCCT 100
DB 209 PLNPBEQFNVLGTPIGCTC 228

RESULT 11
S22395
fetus precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
R:Brown, W.M.; Dziegielewska, K.M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Muelle Eur. J. Biochem. 205, 321-331, 1992
A:Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Commu
A:Reference number: S22394; MUID:92209519
A:Accession: S22395
A:Molecule type: mRNA
A:Residues: 1-362 <BRW>
A:Cross-references: EMBL:X56021; NID:g2104; PIDN:CAA39498.1; PID:g3980229
C:Superfamily: alpha-2-HS-glycoprotein; cystatin homology
C:Keywords: calcium binding; EF hand; glycoprotein
F:1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F:16-362/Product: fetuin #status predicted <MAT>
F:20-134/Domain: cystatin homology <CY1>
F:143-249/Domain: cystatin homology <CY2>
F:96,153,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.3%; Score 75; DB 2; Length 362;
Best Local Similarity 27.6%; Pred. No. 3.3;
Matches 27; Conservative 11; Mismatches 42; Indels 18; Gaps 3;
QY 30 SYDPARYPRYLPEAYCLRCGLTGLFGEDVFRSAPVYMTVVLRRTPACAGRSVYTE 89
DB 210 AYSPKCNLLVEKQYGFCKGTAKVNEEDVATCTVFTOPVLQPPAGA----- 261
QY 90 AYVTIPVGCCTVPEPEKADSNSSI-DKQAKLLG 126
DB 262 ----DAGAT----PVVDAANTASPLADYPAASLVVGP 290

RESULT 12
S28941
coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
N:Alternate names: Hageman factor
C:Species: Cavia porcellus (guinea pig)

C>Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S28941
R:Samba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, Biochim. Biophys. Acta 1159, 113-121, 1992
A:Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage
A:Reference number: S28941; MUID:93003367
A:Accession: S28941
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <SEM>
A:Cross-references: EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolo
C:Keywords: hydrolase; serine proteinase
F:46-87/Domain: fibronectin type II repeat homology <1F2>
F:134-169/Domain: fibronectin type I repeat homology <FBI>
F:177-208/Domain: EGF homology <EGF>
F:216-294/Domain: kringle homology <KRG>
F:359-597/Domain: trypsin homology <TRY>

Query Match 10.3%; Score 75; DB 2; Length 603;
Best Local Similarity 22.2%; Pred. No. 5.7;
Matches 37; Conservative 17; Mismatches 59; Indels 54; Gaps 7;
QY 2 CPAGGRPADRRFRPPT-NLRSVSPWAYRISYDYPARYPRY-----LPEAY 44
DB 60 CIHKRGPGRPMWCATTNFDQDQWAYCL--EPKVKDHCCKHNPQCGGICVNTLSSPH 117
QY 45 CLCRGCLTG-----LFGEDVFRSAPV-----YMTVVL 74
DB 118 CLCPDLTLTKHCQREKCFEPQLHRFFHENEIWFRTGPAVKCHCKGPDHAKCHQMSQEC 177
QY 75 RRTPCAGGRSVYTEAY--VTIPVGCCTVPEPEKADSNSSIDKOG 119
DB 178 QINPCLNGGRGLEVEGHLCDCPMGYT---GPFCDLDTTASCVEGRG 221

RESULT 13
T38292
hypothetical protein SPAC23E2.02 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38292
R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, January 1996
A:Reference number: Z21784
A:Accession: T38292
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1273 <SKE>
A:Cross-references: EMBL:Z68887; PIDN:CAA93114.1; GSPDB:GN00066; SPDB:SPAC23E2.02
A:Experimental source: strain 972h-; cosmid G23E2
C:Genetics:
A:Gene: SPDB:SPAC23E2.02
A:Map position: 1
A:Introns: 8/2; 862/3

Query Match 10.2%; Score 74.5; DB 2; Length 1273;
Best Local Similarity 25.6%; Pred. No. 15;
Matches 22; Conservative 15; Mismatches 48; Indels 1; Gaps 1;
QY 46 LCRGCLTGLFGEDVFRSAPVYMTVVLRRTPACAGRSVYTEAYVTIPVGCCTVPEPE 105
DB 520 ICARQLTGLFSQVSSSFLSKNELPPKVIILEAKERTGGR-IYSRALPVSHTSATQINHHT 578
QY 106 KDADSNSSIDKQGAQKLLGPNDA 131
DB 579 SNSNSISSNSTSLNPKDVTDPDPSHPS 604

RESULT 14
A55535

C;Accession: B81719
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
A;Accession: B81719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <FET>
A;Cross-references: GB:AE002296; GB:AE002160; NID:g7190325; PIDN:AAF39152.1; PID:g7190325
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0284

Query Match 10.4%; Score 76; DB 2; Length 242;
Best Local Similarity 26.2%; Pred. No. 1.7;
Matches 21; Conservative 6; Mismatches 21; Indels 32; Gaps 3;
QY 41 PEAVCLRCGLTGLF-----GEEDVFRSAPVYPTVLLRRTACAGGRSVYT--- 88
DB 161 PEPHCNLCUQIGRIAEEDIEVSEEDLFRSWDI-----SQYGEKMYTVD 208
QY 89 -----EAYVTIPVGCTC 100
DB 209 PLNPEEQFNVLGTPIGCTC 228

RESULT 7
A84663
probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84663
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: A84663
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-509 <SPO>
A;Cross-references: GB:AE002093; NID:g2760830; PIDN:AAB95298.1; GSPDB:GN00139
C;Genetics:
A;Map position: 2

Query Match 10.4%; Score 75.5; DB 2; Length 509;
Best Local Similarity 31.3%; Pred. No. 4.2;
Matches 26; Conservative 16; Mismatches 28; Indels 13; Gaps 5;
QY 48 RGCITGLFGEDVFRSAPVYPTVLLRRTACAGGRSVY-TEAYVTIPVGCTCVPEPEK 106
DB 124 RSKTGSFTEENLEFQK-----ILQRSGL---GESTYLPFAVLNPPN-PCMKEARK 172
QY 107 DADSN-SSIDKQAKLLLGPN 128
DB 173 EAETVMFGAIDELLAKTNVNP 195

RESULT 8
T44254
thiamin biosynthesis protein thic [imported] - Rhizobium etli plasmid b
C;Species: Rhizobium etli
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44254
R;Miranda-Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sob
J. Bacteriol. 179, 6887-6893, 1997
A;Title: Expression of thiamin biosynthetic genes (thiCOGE) and production of symbiotic

A;Reference number: Z22737; MUID:98037482
A;Accession: T44254
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-610 <MIR>
A;Cross-references: EMBL:AF004408; NID:g2627325; PIDN:AAC45972.1; PID:g2627326
A;Experimental source: strain CE3
C;Genetics:
A;Gene: thic
A;Genome: plasmid b
C;Function:
A;Description: involved in the biosynthesis of the pyrimidine moiety of thiamin
C;Superfamily: thiamin biosynthesis protein thic

Query Match 10.4%; Score 75.5; DB 2; Length 610;
Best Local Similarity 29.9%; Pred. No. 5.1;
Matches 38; Conservative 14; Mismatches 54; Indels 21; Gaps 7;
QY 3 PAGRPADRRFRPPTNLRYSVPW---AYRISYDPARYPRYLPEAYCLRCGLTGLFGE-- 57
DB 44 PTSGEPT-----PVTVDSSGPTDPAHVISID-AGLPR-LRESWIKARGDVESYDGRIV 95
QY 58 --EDVFRSAPVYPTVLLRRTPACA-GGRSVYTEAYVTIPVGCTCVPEPEKADDSINSS 114
DB 96 KPEDNGFATGERTPEPPVRNTPLKAKAGRAVTOLAYAR-----AGIVTPEMEFIAIREN 150
QY 115 IDKQAK 121
DB 151 LGRQAQ 157

RESULT 9
D72281
hypothetical protein TM1214 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72281
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
A;Accession: D72281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <ARN>
A;Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36289.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1214
C;Superfamily: psbG protein

Query Match 10.3%; Score 75; DB 2; Length 178;
Best Local Similarity 23.1%; Pred. No. 1.5;
Matches 34; Conservative 12; Mismatches 35; Indels 56; Gaps 7;
QY 18 NLRVSPWAYRISYDPARYPRYLPEAYCLRCG-----LTGLFGEDVFRFSAPV-- 67
DB 13 NLRSRISWMLH-----YCTCGGAVELPPSMTSRFDME--RFGIAPMAT 53
QY 68 -----YMPVTVLRRT-----PACAGGRSVYTEAVT----- 93
DB 54 PRQADILLITGLYTKTLRRVITYTEOMPDPKYVVGFGSGCTINGIYFDSATVNRLDYY 113
QY 94 IPVG---CTCPEPEKADDSINSSIDK 117
DB 114 IPVDVIAGCMRPEAILEAFNYLMEK 140
RESULT 10

Query Match	13.6%;	Score 99;	DB 2;	Length 148;
Best Local Similarity	29.8%;	Pred. No. 0.0038;		
Matches	28:	Conservative	17:	Mismatches 35:
			Indels	14:
			Gaps	5:

QY	20	RSVSPWAYRISVSDARYPRYLPEAYCLRCGC	-LTGLFGEDVDVFRRSPAYMPTVILRR	77
Db	52	RALCPWDSRVNQSRPEKLAESVCLCKRSRGSTGAF	-----CMPIVRKVPILRRV	103
QY	78	PAC--AGGRSVYTEAYVTIPVGC-TCVPEPEKDA		108
Db	104	-SCDRSTGLWNYVRSTELITVGCHSVLPRTORAA		136

```

RESULT      5
T27843
hypothetical protein ZK39.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27843
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20428
A:Accession: T27843
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-226 <WIL>
A:Cross-references: EMBL:Z82093; PIDN:CAB05021.1; GSPDB:GN00019; CESP:ZK39.8
A:Experimental source: clone ZK39
C:Genetics:
A:Gene: CESP:ZK39.8
A:Map position: 1
A:Introns: 32/1; 52/3; 108/1

```

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Query Match          10.8%; Score 78.5; DB 2; Length 226;
Best Local Similarity 25.4%; Pred. No. 0.85;
Matches 31; Conservative 18; Mismatches 32; Indels 41; Gaps 8;

Qy      2 CPAGRRPADRRFPPTNLRYSVPNAYRISYPNAYPRYLPEAYCLRCRC-LTGLEGEDV 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      55 CDAGW---TRFNRP-----GGMCVRVF--PGTYHQPLAESRCOSQAVLTGVQNQEEA 103

Qy      61 RFRSAGVYMPVW-----LRPTACAGRSVYTEAYVTIPGVCFCVPEPKDADSI 111
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      104 K-KTASLLLPQISQSGSIYGLHRTPACSKS-----PISSC-----NSM 143

Qy      112 NS 113
      ||
Db      144 NS 145

```

RESULT 6
B81719
conserved hypothetical protein TC0284 [imported] - Chlamydia muridarum (strain Nigg)
C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence revision 31-Mar-2000 #text change 11-May-2000

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:19:50 ; Search time 14.34 Seconds
(without alignments)
706.500 Million cell updates/sec

Title: US-09-320-713-4_COPY_28_160
Perfect score: 729
Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLLPNDAPAGP 133

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113.5	15.6	147	JC4628	cytotoxic T-lympho
2	108.5	14.9	151	B45351	immediate-early pr
3	108	14.8	150	I49823	cytotoxic T-lympho
4	99	13.6	148	T21334	hypothetical prote
5	78.5	10.8	226	T27843	hypothetical prote
6	76	10.4	242	B81719	conserved hypothet
7	75.5	10.4	509	A84663	probable beta-keto
8	75.5	10.4	610	T44254	thiamin biosynthes
9	75	10.3	178	D72881	hypothetical prote
10	75	10.3	242	A71568	hypothetical prote
11	75	10.3	362	S22395	fetuin precursor -
12	75	10.3	603	S28941	coagulation factor
13	74.5	10.2	1273	T38292	hypothetical prote
14	73	10.0	2397	A55335	versican precursor
15	71.5	9.8	181	I68674	cyclin-dependent k
16	70.5	9.7	181	I54380	cyclin-dependent k
17	70.5	9.7	256	T47860	transcription fact
18	70.5	9.7	265	D70778	hypothetical prote
19	70	9.6	816	C69493	hypothetical prote
20	69.5	9.5	1896	RNF82L	DNA-directed RNA p
21	69	9.5	292	T03122	hypothetical prote
22	68.5	9.4	262	T75093	hypothetical prote
23	68.5	9.4	342	A56552	homeotic protein H
24	68	9.3	173	E71017	probable NADH-ubiq
25	68	9.3	528	T00951	probable 3-oxoacyl
26	67.5	9.3	298	A32872	myogenic factor CM
27	67.5	9.3	872	D75564	probable ATP-depen
28	67	9.2	789	A39564	transcription repr
29	67	9.2	2123	S55089	probable acetyl-Co

30	66.5	9.1	773	2	A71079	probable transcript
31	66.5	9.1	1114	2	T49517	p63 related protei
32	66.5	9.1	1117	2	JC4934	delta-crystallin/E
33	66	9.1	142	2	T51316	probable CO-induce
34	66	9.1	676	2	A40363	DNA ligase (NAD+)
35	65.5	9.0	1316	2	T50444	hypothetical UPF00
36	65	8.9	149	2	A41236	placental growth f
37	65	8.9	170	2	D75115	co-induced hydroge
38	65	8.9	210	2	E70671	hypothetical prote
39	65	8.9	273	2	B86504	CT016 hypothetical
40	65	8.9	273	2	A72120	conserved hypothet
41	65	8.9	329	2	T10064	cytokinin-induced
42	65	8.9	345	1	S56585	L-iditol 2-dehydro
43	65	8.9	345	2	A86135	probable oxidoredu
44	65	8.9	376	2	C70399	S-adenosylmethioni
45	65	8.9	802	2	B43735	bcsB protein - Ace

ALIGNMENTS

RESULT 1
JC4628
cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N;Alternate names: CTLA8 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: JC4628
R;Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.
Gene 168, 223-225, 1996
A;Title: Complete nucleotide sequence of the mouse CTLA8 gene.
A;Reference number: JC4628; MUID:96194901
A;Accession: JC4628
A;Molecule type: DNA
A;Residues: 1-147 <YAO>
A;Cross-references: GB:U35108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500
C;Genetics:
A;Gene: ctla8
A;Introns: 69/2
C;Superfamily: saimiri herpesvirus immediate-early protein 2
C;Keywords: cytokine; glycoprotein; lymphocyte
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-147/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.6%	Score 113.5;	DB 2;	Length 147;
Best Local Similarity	31.4%;	Pred. No. 0.00011;		
Matches	37;	Conservative	16;	Mismatches 46;
		Indels	19;	Gaps 6;
QY	5	GGRPADRRFRPTNLR-RSVSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDVRF	63	
Db	47	GAKVSSR--RPSDYLNKSTSPWTLHRNEDPDYPSVIAEQCRHQRVCNA-EGKLDHNM	103	
QY	64	SAPVIMPTVLLRRTP-ACAGRSVYTYEAYTIPVGCCTCPPEPKDADSIINSIDKQGA	120	
Db	104	SVLQQLLEILVKREPESC---FTFRVEKMLVGVGCTCV-----ASIVRQAA	147	

RESULT 2
B45351
immediate-early protein 2 - saimirine herpesvirus 1 (strain 11)
N;Alternate names: hypothetical protein ORF13
C;Species: saimirine herpesvirus 1
A;Note: Host Saimiri sclerurus (common squirrel monkey)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45351; D36807
R;Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.
Virology 179, 189-200, 1990
A;Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties
A;Reference number: A45351; MUID:91021021
A;Accession: B45351
A;Molecule type: mRNA

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RESULT 14
US-09-854-280-12
; Sequence 12, Application US/09854280
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C2
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL17B-FC fusion
US-09-854-280-12

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; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 4
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-827-4

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Query Match      25.7%   Score 187.5; DB 5; Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

QY 17 TNLRSVPMAYRISYDPARYPLPEAYCLRCGLTGLFGEEDVFRSAPVYMPVTLVR 76
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Db 101 THRSISPRWRYVDTDDEYRQKLAFAECLRCGCDARTGRTAALNSVRLQLSLVLR 160

QY 77 TPACAGGRSVYTEA-----VVTIPVGCTCV 101
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Db 161 RPCSRDGLPTPGAFATFTEFIHVPGCTCV 192

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RESULT 11
US-09-931-836-11
; Sequence 11, Application US/09931836
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
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; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
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; PRIOR FILING DATE: 1999-05-04
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; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
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; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2000-08-22
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; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02

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Db	161	RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV	192
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US-09-480-297A-23			
Sequence 23, Application US/09480297A			
GENERAL INFORMATION:			
APPLICANT: Gorman, Daniel M.			
APPLICANT: Bazan, J. Fernando			
APPLICANT: Kasteleln, Robert A.			
TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS			
FILE REFERENCE: DX0917K			
CURRENT APPLICATION NUMBER: US/09/480,297A			
CURRENT FILING DATE: 2000-01-10			
PRIOR APPLICATION NUMBER: 60/115,506			
PRIOR FILING DATE: 1999-01-11			
NUMBER OF SEQ ID NOS: 34			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 23			
LENGTH: 197			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-480-297A-23			
Query Match	25.7%	Score 187.5; DB 5; Length 197;	
Best Local Similarity	40.2%; Pred. No. 2.6e-11;		
Matches	37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;		
QY	17	TNLRVSPPWARYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDVRFERSAPVYMPVTVLRR	76
Db	101	THORSISPWRIVDTDEDRYPQKLAFAELCRGCGIDARTGRTFAALNSVRLQLSLVLRR	160
QY	77	TPACAGRSVYTEA-----YVTIPVGCTCV	101
Db	161	RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV	192
RESULT	9		
US-09-854-280-3			
Sequence 3, Application US/09854280			
GENERAL INFORMATION:			
APPLICANT: Chen, Jian			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Goddard, Audrey			
APPLICANT: Gurney, Austin			
APPLICANT: Li, Hanzhong			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF			
FILE REFERENCE: P1381R1C2			
CURRENT APPLICATION NUMBER: US/09/854,280			
CURRENT FILING DATE: 2001-05-10			
PRIOR APPLICATION NUMBER: US 09/311,832			
PRIOR FILING DATE: 1999-05-14			
PRIOR APPLICATION NUMBER: US 60/085,579			
PRIOR FILING DATE: 1998-05-15			
PRIOR APPLICATION NUMBER: US 60/113,621			
PRIOR FILING DATE: 1998-12-23			
NUMBER OF SEQ ID NOS: 26			
SEQ ID NO 3			
LENGTH: 197			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-854-280-3			
Query Match	25.7%	Score 187.5; DB 5; Length 197;	
Best Local Similarity	40.2%; Pred. No. 2.6e-11;		
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QY	17	TNLRVSPPWARYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDVRFERSAPVYMPVTVLRR	76
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; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381C1P1C1(US)
; CURRENT APPLICATION NUMBER: US/09/908,827
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134,287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138,387
; PRIOR FILING DATE: 1999-06-09
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; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644,848
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; PRIOR APPLICATION NUMBER: 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000 08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 8
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-827-8

Query Match      *99.5%; Score 725; DB 5; Length 202;
Best Local Similarity 99.2%; Pred. No. 7.8e-65;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 70 SCPAGGRPGDRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 129
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QY 61 RFRSAPVYMPVTVLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKDADSSIDKQGA 120
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Db 130 RFRSAPVYMPVTVLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKDADSSIDKQGA 189
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QY 121 KLLGPNADAPAGP 133
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Db 190 KLLGPNADAPAGP 202
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RESULT 3
US-09-480-297A-6
; Sequence 6, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-6

Query Match      84.1%; Score 613; DB 5; Length 151;
Best Local Similarity 99.1%; Pred. No. 8.1e-54;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 40 SCPAGGRPADRRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 99
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QY 61 RFRSAPVYMPVTVLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKDADSSIN 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 RFRSAPVYMPVTVLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKDADSSIN 151
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RESULT 4
US-09-480-297A-12
; Sequence 12, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:19:50 ; Search time 16.65 seconds
(without alignments)
377.498 Million cell updates/sec

Title: US-09-320-713-4_COPY_28_160
Perfect score: 729
Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLGPNDAPAGP 133

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 309837 seqs, 47258215 residues

Total number of hits satisfying chosen parameters: 309837

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	100.0	202	5	US-09-480-297A-8
2	725	99.5	202	5	US-09-908-827-8
3	613	84.1	151	5	US-09-480-297A-6
4	601	82.4	205	5	US-09-480-297A-12
5	208	28.5	44	5	US-09-480-297A-10
6	193	26.5	425	5	US-09-854-280-13
7	187.5	25.7	197	5	US-09-886-404-8
8	187.5	25.7	197	5	US-09-480-297A-23
9	187.5	25.7	197	5	US-09-854-280-3
10	187.5	25.7	197	5	US-09-908-827-4
11	187.5	25.7	197	5	US-09-931-836-11
12	187.5	25.7	197	6	US-60-309-936-2
13	187.5	25.7	206	5	US-09-854-280-24
14	176.5	24.2	408	5	US-09-854-280-12
15	174	23.9	117	5	US-09-886-404-7
16	174	23.9	175	5	US-09-854-280-23
17	174	23.9	180	5	US-09-480-297A-2
18	174	23.9	180	5	US-09-854-280-1
19	174	23.9	180	5	US-09-908-827-2
20	174	23.9	180	5	US-09-929-404-150
21	173	23.7	180	5	US-09-480-297A-4
22	169	23.2	117	5	US-09-886-404-6
23	155.5	21.3	163	5	US-09-908-827-10
24	139.5	19.1	123	5	US-09-480-297A-21
25	130.5	17.9	155	5	US-09-886-404-5
26	130.5	17.9	155	5	US-09-480-297A-33
27	130.5	17.9	155	5	US-09-854-280-11

28	119.5	16.4	78	5	US-09-864-761-35772	Sequence 35772, A
29	114.5	15.7	159	5	US-09-886-404-10	Sequence 10, Appl
30	114.5	15.7	169	5	US-09-886-404-4	Sequence 4, Appl
31	114.5	15.7	169	5	US-09-480-297A-18	Sequence 18, Appl
32	114.5	15.7	169	5	US-09-836-385-4	Sequence 4, Appl
33	113.5	15.6	147	5	US-09-480-297A-32	Sequence 32, Appl
34	110.5	15.2	161	5	US-09-886-404-2	Sequence 2, Appl
35	110.5	15.2	161	5	US-09-480-297A-14	Sequence 14, Appl
36	110.5	15.2	161	5	US-09-836-385-2	Sequence 2, Appl
37	110.5	15.2	177	5	US-09-908-827-6	Sequence 6, Appl
38	108.5	14.9	151	5	US-09-480-297A-34	Sequence 34, Appl
39	108	14.8	150	5	US-09-480-297A-31	Sequence 31, Appl
40	105.5	14.5	144	5	US-09-480-297A-16	Sequence 16, Appl
41	104.5	14.3	183	5	US-09-760-476-2515	Sequence 2515, Ap
42	97.5	13.4	111	5	US-09-480-297A-26	Sequence 26, Appl
43	94	12.9	350	1	PCT-US01-08631-59731	Sequence 59731, A
44	75.5	10.4	513	5	US-09-573-655A-1267	Sequence 1267, Ap
45	75	10.3	393	1	PCT-US01-08631-50536	Sequence 50536, A

ALIGNMENTS

RESULT 1

US-09-480-297A-8
; Sequence 8, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-8

Query Match 100.0%; Score 729; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 3.le-65;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEDV 60
Db 70 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEDV 129
Qy 61 RFRSAPVMTVLLRRTPACAGGRSVYTYAVTIPVCGTCVPEPEKDADSISSIDKQGA 120
Db 130 RFRSAPVMTVLLRRTPACAGGRSVYTYAVTIPVCGTCVPEPEKDADSISSIDKQGA 189
Qy 121 KLLGPNDAFAGP 133
Db 190 KLLGPNDAFAGP 202

RESULT 2

US-09-908-827-8
; Sequence 8, Application US/09908827
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin

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; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-4

Query Match          100.0%; Score 729; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
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Db 54 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 113
   |||
QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   |||
Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   |||
QY 121 KLLGPNADAPAGP 133
Db 174 KLLGPNADAPAGP 186

RESULT 13
US-09-397-846-4
; Sequence 4, Application US/09397846
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846
; CURRENT FILING DATE: 1999-09-17
; EARLIER APPLICATION NUMBER: 60/100,706
; EARLIER FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846-4

Query Match          100.0%; Score 729; DB 17; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
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Db 54 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 113
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QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
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Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   |||
QY 121 KLLGPNADAPAGP 133
Db 174 KLLGPNADAPAGP 186

RESULT 14
US-09-397-846B-4
; Sequence 4, Application US/09397846B
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846B
; CURRENT FILING DATE: 2001-05-21
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; PRIOR APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846B-4

Query Match          100.0%; Score 729; DB 17; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   |||
Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   |||
QY 121 KLLGPNADAPAGP 133
Db 174 KLLGPNADAPAGP 186

RESULT 15
US-09-154-817-3
; Sequence 3, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-3

Query Match          100.0%; Score 729; DB 15; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
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Db 55 SCGAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 114
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QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
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Db 115 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 174
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QY 121 KLLGPNADAPAGP 133
Db 175 KLLGPNADAPAGP 187

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Job time: 187 sec
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Best Local Similarity 100.0%; Pred. No. 1.5e-73;
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Db 41 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 100
QY 61 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 101 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 160
QY 121 KLLGPNADAPAGP 133
Db 161 KLLGPNADAPAGP 173

RESULT 9
US-09-154-817-5
; Sequence 5, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; APPLICANT: Foley, Kevin
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-5

Query Match      100.0%; Score 729; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 10
US-09-397-846-5
; Sequence 5, Application US/09397846
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846-5
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US-09-397-846-5

Query Match      100.0%; Score 729; DB 17; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 11
US-09-397-846B-5
; Sequence 5, Application US/09397846B
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846B-5

Query Match      100.0%; Score 729; DB 17; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTPCAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 12
US-09-154-817-4
; Sequence 4, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; APPLICANT: Foley, Kevin
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
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RESULT 7
US-09-320-713-32
; Sequence 32, Application US/09320713
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-320-713-32

Query Match 100.0%; Score 729; DB 17; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 SCPAGGRPADRRFPPTNLSRSPWAYRISYDPAHYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 41 SCPAGGRPADRRFPPTNLSRSPWAYRISYDPAHYPRYLPEAYCLRCGLTGLFGEEDV 100

Qy 61 RFRSAPYMTVTVLRRTPACAGRSYVTEAYVTPVGCCTCVPEPKDADSISSIDKQGA 120
Db 101 RFRSAPYMTVTVLRRTPACAGRSYVTEAYVTPVGCCTCVPEPKDADSISSIDKQGA 160

Qy 121 KLLGPNADAPGP 133
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RESULT 8
US-09-731-816-32
; Sequence 32, Application US/09731816
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/09/731,816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-32

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; Sequence 4, Application PC/TUS9911644				
; GENERAL INFORMATION:				
; APPLICANT : Human Genome Sciences, Inc.				
; TITLE OF INVENTION : INTERLEUKINS -21 AND 22				
; FILE REFERENCE : PF470PCT				
; CURRENT APPLICATION NUMBER : PCT/US99/11644				
; CURRENT FILING DATE : 1999-05-27				
; EARLIER APPLICATION NUMBER : 60/087,340				
; EARLIER FILING DATE : 1998-05-29				
; EARLIER APPLICATION NUMBER : 60/099,805				
; EARLIER FILING DATE : 1998-09-10				
; EARLIER APPLICATION NUMBER : 60/131,965				
; EARLIER FILING DATE : 1999-04-30				
; NUMBER OF SEQ ID NOS : 32				
; SOFTWARE : PatentIn Ver. 2.0				
; SEQ ID NO 4				
; LENGTH : 160				
; TYPE : PRT				
; ORGANISM : Homo sapiens				
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QY	61	RFRSAPVMPVTVLRRTPACAGGRSVYTEAVYTIPVGTCVPEPEKDDADSSINSSIDKQGA	120	
Db	88	RFRSAPVMPVTVLRRTPACAGGRSVYTEAVYTIPVGTCVPEPEKDDADSSINSSIDKQGA	147	
QY	121	KLLGPNDA	PAGP	133
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; Sequence 12, Application US/09231788A				
; GENERAL INFORMATION:				
; APPLICANT : Ebner, Reinhard				
; TITLE OF INVENTION : Interleukin-20				
; FILE REFERENCE : PF399pl				
; CURRENT APPLICATION NUMBER : US/09/231,788A				
; CURRENT FILING DATE : 1999-01-15				
; EARLIER APPLICATION NUMBER : 60/052,870				
; EARLIER FILING DATE : 1997-07-16				
; EARLIER APPLICATION NUMBER : 60/055,952				
; EARLIER FILING DATE : 1997-08-18				
; EARLIER APPLICATION NUMBER : 60/060,140				
; EARLIER FILING DATE : 1997-09-26				
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Db	28	SCPAGGRPADRRFPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	87						
Qy	61	RFRSAPVYMTVTLRRTTACAGGRSVYTEAYVTIPVGCTCVPPEPKDADSINSSIDKQGA	120						
Db	88	RFRSAPVYMTVTLRRTTACAGGRSVYTEAYVTIPVGCTCVPPEPKDADSINSSIDKQGA	147						
Qy	121	KLLIGPNDAPAGP	133						
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;	GENERAL INFORMATION:								
;	APPLICANT: Reinhard Ebner								
;	APPLICANT: Steven M. Ruben								
;	TITLE OF INVENTION: INTERLEUKINS-21 AND 22								
;	FILE REFERENCE: PF470								
;	CURRENT APPLICATION NUMBER: US/09/320,713								
;	CURRENT FILING DATE: 1999-05-27								
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;	EARLIER FILING DATE: 1998-05-29								
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;	EARLIER FILING DATE: 1998-09-10								
;	EARLIER APPLICATION NUMBER: 60/131,965								
;	EARLIER FILING DATE: 1999-04-30								
;	NUMBER OF SEQ ID NOS: 32								
;	SOFTWARE: PatentIn Ver. 2.0								
;	SEQ ID NO 4								
;	LENGTH: 160								
;	TYPE: PRT								
;	ORGANISM: Homo sapiens								
US-09-320-713-4									
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Db	28	SCPAGGRPADRRFPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	87						
Qy	61	RFRSAPVYMTVTLRRTTACAGGRSVYTEAYVTIPVGCTCVPPEPKDADSINSSIDKQGA	120						
Db	88	RFRSAPVYMTVTLRRTTACAGGRSVYTEAYVTIPVGCTCVPPEPKDADSINSSIDKQGA	147						
Qy	121	KLLIGPNDAPAGP	133						
Db	148	KLLIGPNDAPAGP	160						
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;	Sequence 4, Application US/09731816								
;	GENERAL INFORMATION:								
;	APPLICANT: Ebner, Reinhard								
;	APPLICANT: Ruben, Steven								
;	TITLE OF INVENTION: Interleukins-21 and 22								
;	FILE REFERENCE: PF470P1								
;	CURRENT APPLICATION NUMBER: US/09/731,816								
;	CURRENT FILING DATE: 2000-12-08								
;	PRIOR APPLICATION NUMBER: 60/169,837								
;	PRIOR FILING DATE: 1999-12-09								
;	PRIOR APPLICATION NUMBER: 09/320,713								
;	PRIOR FILING DATE: 1999-05-27								
;	PRIOR APPLICATION NUMBER: 60/087,340								
;	PRIOR FILING DATE: 1998-05-29								

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Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	729	100.0	160	17	US-09-320-713-4
5	729	100.0	160	21	US-09-731-816-4
6	729	100.0	173	1	PCT-US99-11644-32
7	729	100.0	173	1	US-09-320-713-32
8	729	100.0	173	21	US-09-731-816-32
9	729	100.0	185	15	US-09-154-817-5
10	729	100.0	185	17	US-09-397-846-5

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23	729	100.0	209	17	US-09-397-846-17	Sequence 17, Appli
24	729	100.0	209	17	US-09-397-846B-17	Sequence 17, Appli
25	725	99.5	202	21	US-09-747-259-8	Sequence 8, Appli
26	725	99.5	202	22	US-09-816-744-8	Sequence 8, Appli
27	601	82.4	183	17	US-09-397-846-12	Sequence 12, Appli
28	601	82.4	183	17	US-09-397-846B-12	Sequence 12, Appli
29	601	82.4	205	17	US-09-397-846-9	Sequence 9, Appli
30	601	82.4	205	17	US-09-397-846B-9	Sequence 9, Appli
31	601	82.4	205	21	US-09-724-864-37	Sequence 37, Appli
32	303	41.6	57	17	US-09-397-846-21	Sequence 21, Appli
33	303	41.6	57	17	US-09-397-846B-21	Sequence 21, Appli
34	242	33.2	54	17	US-09-397-846-19	Sequence 19, Appli
35	242	33.2	54	17	US-09-397-846B-19	Sequence 19, Appli
36	193	26.5	425	17	US-09-311-832-13	Sequence 13, Appli
37	187.5	25.7	179	16	US-09-283-810-3	Sequence 3, Appli
38	187.5	25.7	197	1	PCT-US99-11644-29	Sequence 29, Appli
39	187.5	25.7	197	16	US-09-283-810-2	Sequence 2, Appli
40	187.5	25.7	197	17	US-09-311-832-3	Sequence 3, Appli
41	187.5	25.7	197	17	US-09-320-713-29	Sequence 29, Appli
42	187.5	25.7	197	18	US-09-409-441-2	Sequence 2, Appli
43	187.5	25.7	197	21	US-09-731-816-29	Sequence 29, Appli
44	187.5	25.7	197	21	US-09-747-259-4	Sequence 4, Appli
45	187.5	25.7	197	23	US-60-266-159-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
PCT-US00-00807-12
; Sequence 12, Application PC/TUS00000807
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399PCY2
; CURRENT APPLICATION NUMBER: PCT/US00/00807
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 09/231,788
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-00807-12

Query Match 100.0%; Score 729; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SCFAGGRRPDRRPPPTNLR	SVSPWAYRISYDPA	RYPRYLPEAYCLRCGLTGLFGEDV	60
Db	28	SCFAGGRRPDRRPPPTNLR	SVSPWAYRISYDPA	RYPRYLPEAYCLRCGLTGLFGEDV	87
QY	61	RFRSAPYMTVVLRRTP	PACAGGRSVTEAYVTIP	VGCTCVPEPEKADSI	120
Db	88	RFRSAPYMTVVLRRTP	PACAGGRSVTEAYVTIP	VGCTCVPEPEKADSI	147
QY	121	KLILGPNDAPAG	PAGP		133

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; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8

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```

Query Match      14.9%; Score 108.5; DB 3; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

QY  20 RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDVRFERSADPVYMPVTVLRRTPA 79
    ||||| : |||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db   65 RSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEILVVRK--- 120
    ||||| : |||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY  80 CAGGRSVYTEAY----VTIPVGCTCV 101
    | : : |||||
Db  121 ---GHQPCPNFRLKMLVTVGCTCV 143

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Search completed: October 5, 2001, 15:20:11
 Job time: 21 sec


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; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-257-7

Query Match 15.4%; Score 112; DB 4; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFPNNL-RVSPWAYRISYDPARYLPAYCLRCGLTGLFGEEDVRF 63
| : : | | | | | | | | : : | | | : : | : | : | : |
Db 58 GAKVSSR--RPSDYLNKSTSPWTLHRNEDPDYPSVIWEAQRHRCVNA-EGKLDHNM 114
| : : | | | | | : : : : : | : : | : : | : : | : : |
QY 64 SAPVYPTVVLRRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
| : : | | | | | : : : : : | : : | : : | : : | : : |
Db 115 SVLIQQLVILVKREPESCP---FTFRVEKMLVGVGCTCV 150

RESULT 12
US-08-620-694A-8
; Sequence 8, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-08-620-694A-8

Query Match 14.9%; Score 108.5; DB 2; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

QY 20 RSVSPWAYRISYDPARYLPAYCLRCGLTGLFGEEDVRFSAFVYPTVVLRRTPA 79
| : : | | | | | | | | : : | | | : : | : | : | : |
Db 65 RSTSPWTLHRNEDPDYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQCEILVWRK--- 120
| : : | | | | | : : : : : | : : | : : | : : | : : |
QY 80 CAGGRSVYTEAY---VTIPVGCTCV 101
| : : | | | | | : : : : : | : : | : : | : : | : : |
Db 121 ---GHQPCPNFSRLEKMLVTVGCTCV 143

RESULT 13
US-09-034-810-6
; Sequence 6, Application US/09034810
; Patent No. 6043344
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden/Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDDPYPSVIWEAQCRHRCVNA-EGKLDHNM 114
QY 64 SAPVYMTVTLRRTP-ACAGRSVYTEAYTIPVGCTCV 101
; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 115 SVLIQQLVLRKREPSCP---FTFRVEKMLVGVGCTCV 150

RESULT 9
US-09-022-260-7
; Sequence 7, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-260-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDVRF 63
; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDDPYPSVIWEAQCRHRCVNA-EGKLDHNM 114
QY 64 SAPVYMTVTLRRTP-ACAGRSVYTEAYTIPVGCTCV 101
; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 115 SVLIQQLVLRKREPSCP---FTFRVEKMLVGVGCTCV 150

RESULT 10
US-09-022-259-7
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```

; Sequence 7, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-259-7

Query Match 15.4%; Score 112; DB 4; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDVRF 63
; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDDPYPSVIWEAQCRHRCVNA-EGKLDHNM 114
QY 64 SAPVYMTVTLRRTP-ACAGRSVYTEAYTIPVGCTCV 101
; : : | | | | | | | | | | : : | | | : | | : | : | : | : | : | : |
Db 115 SVLIQQLVLRKREPSCP---FTFRVEKMLVGVGCTCV 150

RESULT 11
US-09-022-257-7
; Sequence 7, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
```

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; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDPDYPSVWEAQCRHRCVNA-EGKLDHNM 114

QY 64 SAPYMPVTVLLRTP-ACAGRSVYTEAYVTIPVGCTCV 101
Db 115 SVLIQIEILVKREPESCP---FTFRVEKMLVGVGCTCV 150

RESULT 7
US-09-022-696-7
; Sequence 7, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-022-696-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDPDYPSVWEAQCRHRCVNA-EGKLDHNM 114

QY 64 SAPYMPVTVLLRTP-ACAGRSVYTEAYVTIPVGCTCV 101
Db 115 SVLIQIEILVKREPESCP---FTFRVEKMLVGVGCTCV 150

RESULT 8
US-09-022-253-7
; Sequence 7, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63

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; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,239
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-685-239-2

Query Match 21.3%; Score 155.5; DB 3; Length 163;
Best Local Similarity 36.0%; Pred. No. 1.3e-10;
Matches 41; Conservative 15; Mismatches 41; Indels 17; Gaps 6;
QY 1 SC---PAGGRPAD-----RRPRPNL--RSVSPWAYRISYDPARYPLPEAYCLCR 48
DB 46 SCPVPGGSKLDIGIENQORVMSNRNIESRSTSPWNYVTWDPNRPSEVVOAQRNL 105
QY 49 GCLGLFGEDVFRSPAPVYMTVVLRRTPACAGRSV-YTEAYVTIPVGCTCV 101
DB 106 GCINAQ-GKEDISMNSVPIQOETLVRRKHQ---GCSVSFQLEKVLVTVGCTCV 155

RESULT 5
US-08-620-694A-7
; Sequence 7, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-620-694A-7
Query Match 15.4%; Score 112; DB 2; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;
QY 5 GGRPADRRFRPTNL-RSVSPWAYRISYDPARYPLPEAYCLRGCLTGLFGEDVFR 63
DB 58 GAKVSSR-RPSDYLNRESTSPWTLHRNEDPDYPSVIWEAQCRHRCVNA-EGKLDHNM 114
QY 64 SAPVYMTVVLRRTP-ACAGRSVYTEAYVTIPVGCTCV 101
DB 115 SVLIQQEILLVKREPESCP---FTFRVEKMLVGVGCTCV 150
RESULT 6
US-09-022-255-7
; Sequence 7, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	155.5	21.3	153	1	US-08-514-014-12	Sequence 12, Appl
2	155.5	21.3	153	2	US-08-833-823-12	Sequence 12, Appl
3	155.5	21.3	163	3	US-09-034-810-2	Sequence 2, Appl
4	155.5	21.3	163	3	US-08-685-239-2	Sequence 2, Appl
5	112	15.4	158	2	US-08-620-694A-7	Sequence 7, Appl
6	112	15.4	158	3	US-09-022-255-7	Sequence 7, Appl
7	112	15.4	158	3	US-09-022-696-7	Sequence 7, Appl
8	112	15.4	158	3	US-09-022-253-7	Sequence 7, Appl
9	112	15.4	158	3	US-09-022-260-7	Sequence 7, Appl
10	112	15.4	158	4	US-09-022-259-7	Sequence 7, Appl
11	112	15.4	158	4	US-09-022-257-7	Sequence 7, Appl
12	108.5	14.9	151	2	US-08-620-694A-8	Sequence 8, Appl
13	108.5	14.9	151	3	US-09-034-810-6	Sequence 6, Appl
14	108.5	14.9	151	3	US-09-022-255-8	Sequence 8, Appl
15	108.5	14.9	151	3	US-09-022-696-8	Sequence 8, Appl
16	108.5	14.9	151	3	US-08-685-239-6	Sequence 6, Appl
17	108.5	14.9	151	3	US-09-022-253-8	Sequence 8, Appl
18	108.5	14.9	151	3	US-09-022-260-8	Sequence 8, Appl
19	108.5	14.9	151	4	US-09-022-259-8	Sequence 8, Appl
20	108.5	14.9	151	4	US-09-022-257-8	Sequence 8, Appl
21	108	14.8	150	3	US-09-034-810-4	Sequence 4, Appl
22	108	14.8	150	3	US-08-685-239-4	Sequence 4, Appl
23	75	10.3	361	2	US-08-483-926A-9	Sequence 9, Appl
24	72	9.9	397	5	PCT-US94-09700-11	Sequence 11, Appl
25	71.5	9.8	164	1	US-07-970-462A-2	Sequence 2, Appl
26	71.5	9.8	164	1	US-08-154-915-6	Sequence 6, Appl
27	71.5	9.8	164	1	US-08-406-248-2	Sequence 2, Appl


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FT Modified-site /note= "phosphorylation site"
FT 164..166
FT /note= "N-glycosylation site"
FT Modified-site 166..168
FT /note= "calcium phosphorylation site"
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XX WO200042188-A2.
XX
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000006.
XX
XX 11-JAN-1999; 99US-02288322.
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
PI WPI; 2000-466130/40.
DR N-PSDB; AAA58985.
XX
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like
PT protein used to identify genes for homologous proteins -
XX
XX Claim 11; Page 15-16; 11lpp; English.
XX
XX The present sequence represents an interleukin-173 (IL-173) polypeptide.
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
CC member of a new group of interleukins, IL-170 polypeptides. The members
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
CC protein can be used to treat abnormal proliferation e.g. cancer
CC or degenerative conditions. Antibodies can be used in diagnostic
CC methods to detect over production of IL-170 protein in cells or body
CC fluids.
XX
XX Sequence 205 AA;
SQ
Query Match 82.4%; Score 601; DB 21; Length 205;
Best Local Similarity 83.3%; Pred. No. 4.5e-60;
Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
QY 1 SCPAGGRPADRRPPTNLRKSPWARYISYDPARYPRVLPAYCLRCGLTGLFGEEDV 60
DB 77 scpagraadrfrfptnrlrsrswaryisyparprylpeayclrcgltglyceedf 136
QY 61 RFRSAPVYMTVLRTPACAGRSVYTYAYVTIPVGCCTCVPPEKADDSINSSIDKQGA 120
DB 137 rfrstpvspavvlrrtaacaggrsvyaehyitipvgctcvpepdkdsadsansmd--- 192
QY 121 KLLLGPNAPAG 132
DB 193 klllgpadrpag 204
RESULT 15
AAB07691
ID AAB07691 standard; Protein; 205 AA.
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XX AAB07691;
XX
XX 07-NOV-2000 (first entry)
XX
XX A murine interleukin-173 polypeptide.
XX
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
KW IL-174; IL-176; IL-177; cell proliferation; cancer; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /note= "signal peptide"

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FT Modified-site 4..6
FT /note= "protein kinase C phosphorylation site"
FT 25..205
FT /note= "mature protein"
FT Modified-site 50..53
FT /note= "cAMP protein kinase site"
FT Modified-site 50
FT /note= "phosphorylation site"
FT Modified-site 53
FT /note= "phosphorylation site"
FT Modified-site 51..53
FT /note= "N-glycosylation site"
FT Modified-site 57..61
FT /note= "myristoylation site"
FT Modified-site 66..69
FT /note= "cAMP protein kinase site"
FT Modified-site 72..75
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FT Modified-site 75
FT /note= "phosphorylation site"
FT Modified-site 80
FT /note= "phosphorylation site"
FT Modified-site 82
FT /note= "phosphorylation site"
FT Modified-site 82..84
FT /note= "calcium phosphorylation site"
FT Modified-site 101..105
FT /note= "myristoylation site"
FT Modified-site 113
FT /note= "phosphorylation site"
FT Modified-site 113..116
FT /note= "cAMP protein kinase site"
FT Modified-site 116
FT /note= "phosphorylation site"
FT Modified-site 159..161
FT /note= "calcium phosphorylation site"
FT Modified-site 164..166
FT /note= "N-glycosylation site"
FT Modified-site 166..168
FT /note= "calcium phosphorylation site"
XX WO200042187-A1.
XX
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US000005.
XX
XX 11-JAN-1999; 99US-0229402.
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
PI WPI; 2000-476060/41.
DR N-PSDB; AAA59157.
XX
XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated
PT interleukin-171 (IL-171), useful for recombinant production of IL-171
PT which can be used for treating conditions associated with abnormal
PT physiology or development -
XX
XX Disclosure; Page 17-18; 11lpp; English.
XX
XX The present sequence represents an interleukin (IL)-173 polypeptide.
CC It is a mammalian homologue of the cytokine designated CTLA-8 (also
CC referred to as IL-17). The specification also describes homologues
CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
CC sequence encoding IL-171 is useful for identifying genes, mRNA and
CC cDNA molecules which code for related or homologous proteins. The
CC IL-171 protein, antibodies against IL-171, and compounds which have
CC binding affinity to IL-171 are useful in treatment of conditions

```


PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated
PT Interleukin-171 (IL-171), useful for recombinant production of IL-171
PT which can be used for treating conditions associated with abnormal
PT physiology or development -
XX
PS Disclosure; Page 97; 111pp; English.
XX
CC The present sequence represents an interleukin (IL)-173 polypeptide.
CC It is a mammalian homologue of the cytokine designated CTLA-8 (also
CC referred to as IL-17). The specification also describes homologues
CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
CC sequence encoding IL-171 is useful for identifying genes, mRNA and
CC cDNA molecules which code for related or homologous proteins. The
CC IL-171 protein, antibodies against IL-171, and compounds which have
CC binding affinity to IL-171 are useful in treatment of conditions
CC associated with abnormal physiology or development, including abnormal
CC proliferation, e.g. cancerous conditions, or degenerative conditions.
CC The IL-171 protein can be used in kits and assay methods for identifying
CC compounds that selectively bind to IL-171.
XX
SQ Sequence 151 AA;

Query Match 84.1%; Score 613; DB 21; Length 151;
Best Local Similarity 99.1%; Pred. No. 1.4e-61;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 40 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 99
QY 61 RFRSAPVYMTVVLRTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDIN 112
Db 100 RFRSAPVYMTVVLRTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDIN 151

RESULT 13
AAY70658
ID AAY70658 standard; Protein; 183 AA.
XX
AC AAY70658;
XX
DT 18-JUL-2000 (first entry)
XX
DE Mature murine transforming growth factor beta-9, Ztgbeta-9 protein.
XX
KW Murine transforming growth factor beta-9; Ztgbeta-9;
KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW antiviral; cytostatic.
XX
OS Mus sp.
XX
PN WO200015798-A2.
XX
PD 23-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US21677.
XX
PR 17-SEP-1998; 98US-O154817.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Taft DW, Foley KP;
XX
DR WPI: 2000-271436/23.
DR N-PSDB; AA252198.
XX
XX Polynucleotides encoding a novel transforming growth factor beta-9
PT polypeptide, designated Ztgbeta-9, useful as an antiviral and
PT antiproliferative agent -
XX

PS Claim 6; Page 89; 97pp; English.
XX
CC The present sequence is the mature murine transforming growth factor
CC beta-9 designated Ztgbeta-9. The signal sequence extends from
CC amino acid residues 1 to 22. Murine Ztgbeta-9 was found to be highly
CC expressed in the HCL hypothalamic cell line. This can be used
CC to treat a variety of neurodegenerative diseases such as amyotrophic
CC lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease,
CC Parkinson's disease and peripheral neuropathies, or demyelinating
CC diseases including multiple sclerosis. Ztgbeta-9 peptides have
CC antiviral activity and may also be used to regulate the proliferation,
CC differentiation and apoptosis of neurons, glial cells, lymphocytes,
CC hematopoietic cells and stromal cells.
XX
SQ Sequence 183 AA;

Query Match 82.4%; Score 601; DB 21; Length 183;
Best Local Similarity 83.3%; Pred. No. 3.9e-60;
Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
QY 1 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 55 SCPAGGRPADRRFRPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 114
QY 61 RFRSAPVYMTVVLRTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDINSSIDKQGA 120
Db 115 RFRSAPVYMTVVLRTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDINSSIDKQGA 170
QY 121 KLLLGPNADAPAG 132
Db 171 KLLLGPNADAPAG 182

RESULT 14
AAB07597
ID AAB07597 standard; Protein; 205 AA.
XX
AC AAB07597;
XX
DT 07-NOV-2000 (first entry)
XX
DE A murine interleukin (IL) 173 polypeptide.
XX
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW IL-177; IL-171; cell proliferation; cancer.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 /note= "signal peptide"
FT Protein 25..205 /note= "mature protein"
FT Modified-site 50 /note= "phosphorylation site"
FT Modified-site 51..53 /note= "N-glycosylation site"
FT Modified-site 53 /note= "phosphorylation site"
FT Modified-site 57..61 /note= "phosphorylation site"
FT Modified-site 80 /note= "myristoylation site"
FT Modified-site 82 /note= "phosphorylation site"
FT Modified-site 82..84 /note= "phosphorylation site"
FT Modified-site 101..105 /note= "calcium phosphorylation site"
FT Modified-site 113 /note= "myristoylation site"
FT Modified-site 116 /note= "phosphorylation site"

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FH Key      Location/Qualifiers
FT Peptide  1..22
FT          /label= Signal_peptide
XX
XX WO200015798-A2.
XX
XX 23-MAR-2000.
XX
XX 17-SEP-1999; 99WO-US21677.
XX
XX 17-SEP-1998; 98US-0154817.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Taft DW, Foley KP;
XX
XX WPI; 2000-271436/23.
XX
XX N-PSDB; AA252201.
XX
XX Polynucleotides encoding a novel transforming growth factor beta-9
XX polypeptide, designated ztgf beta-9, useful as an antiviral and
XX antiproliferative agent
XX
XX Claim 6; Page 92-93; 97pp; English.
XX
XX The present sequence is a variant of human transforming growth
XX factor beta-9, designated ztgf beta-9. Human ztgf beta-9 was isolated
XX from an arrayed pituitary gland cDNA plasmid library by PCR screening.
XX This can be used to treat a variety of neurodegenerative diseases such
XX as anyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's
XX disease, Parkinson's disease and peripheral neuropathies, or
XX demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides
XX have antiviral activity and may also be used to regulate the
XX proliferation, differentiation and apoptosis of neurons, glial cells,
XX lymphocytes, hematopoietic cells and stromal cells.
XX
XX Sequence 209 AA;

Query Match      100.0%; Score 729; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFPPTNLSVSPWAYRISYDPARYPLPEAYCLRCGLTGLFGEDV 60
Db 77 scpaggrpadrrfpptnlrsvspwayrissydparypyleayclrcgltglfgeedv 136

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTIPVGTCTVPEPEKDADSI 120
Db 137 rfrsapvymptvvlrrtpacaggrsvyteayvtipvgctcvpepekadsinsidkqga 196

QY 121 KLLGLPNDAFAGP 133
Db 197 kllglpndafagp 209

RESULT 11
AAB07594
ID AAB07594 standard; Protein; 151 AA.
XX
XX AAB07594;
XX
XX 07-NOV-2000 (first entry)
XX
XX A human interleukin (IL) 173 polypeptide.
XX
XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
XX IL-177; IL-171; cell proliferation; cancer.
XX
XX Homo sapiens.
XX
XX WO200042188-A2.
XX

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PD 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US00006.
XX
XX 11-JAN-1999; 99US-0228822.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-466130/40.
XX
XX N-PSDB; AAA58982.
XX
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like
XX protein used to identify genes for homologous proteins
XX
XX Claim 11; Page 12-13; 111pp; English.
XX
XX The present sequence represents an interleukin-173 (IL-173) polypeptide.
XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
XX member of a new group of interleukins IL-170 polypeptides. The members
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX protein can be used to treat abnormal proliferation e.g. cancer
XX or degenerative conditions. Antibodies can be used in diagnostic
XX methods to detect over production of IL-170 protein in cells or body
XX fluids.
XX
XX Sequence 151 AA;

Query Match      84.1%; Score 613; DB 21; Length 151;
Best Local Similarity 99.1%; Pred. No. 1.4e-61;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFPPTNLSVSPWAYRISYDPARYPLPEAYCLRCGLTGLFGEDV 60
Db 40 scpaggrpadrrfpptnlrsvspwayrissydparypyleayclrcgltglfgeedv 99

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTIPVGTCTVPEPEKDADSI 112
Db 100 rfrsapvymptvvlrrtpacaggrsvyteayvtipvgctcvpepekadsin 151

RESULT 12
AAB07690
ID AAB07690 standard; Protein; 151 AA.
XX
XX AAB07690;
XX
XX 07-NOV-2000 (first entry)
XX
XX A rat interleukin-173 polypeptide.
XX
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
XX IL-174; IL-176; IL-177; cell proliferation; cancer.
XX
XX Rattus sp.
XX
XX WO200042187-A1.
XX
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US00005.
XX
XX 11-JAN-1999; 99US-0229402.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-476060/41.
XX
XX N-PSDB; AAA59156.
XX

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XX 10-JAN-2000; 2000WO-US00005.
 XX 11-JAN-1999; 99US-0229402.
 XX (SCHE) SCHERING CORP.
 XX Gorman DM, Bazan JF, Kastelein RA;
 XX WPI: 2000-476060/41.
 XX N-PSDB; AAA59155.
 XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated
 PT interleukin-171 (IL-171), useful for recombinant production of IL-171
 PT which can be used for treating conditions associated with abnormal
 PT physiology or development -
 XX Disclosure; Page 16-17; 111pp; English.
 XX The present sequence represents an interleukin (IL)-173 polypeptide.
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also
 CC referred to as IL-17). The specification also describes homologues
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and
 CC cDNA molecules which code for related or homologous proteins. The
 CC IL-171 protein, antibodies against IL-171, and compounds which have
 CC binding affinity to IL-171 are useful in treatment of conditions
 CC associated with abnormal physiology or development, including abnormal
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.
 CC The IL-171 protein can be used in kits and assay methods for identifying
 CC compounds that selectively bind to IL-171.
 XX Sequence 202 AA;
 SQ
 Query Match 100.0%; Score 729; DB 21; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.5e-74;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCPAGGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
 DB 70 scpaggrpadrrpptnlrsvspwayrissydparyprylpeayclrcgltlgfeadv 129
 QY 61 RFRSAPVYMTVVLRTPACAGRSVYTEAYVTIPVGCCTCPEPEKADBSINSSIDKQGA 120
 DB 130 rfrsapvymptvvlrrtpacagrsvyteayvtipvgctcpepekadsinsidkqga 189
 QY 121 KLLGPNDAAGP 133
 DB 190 killgpnadapagp 202
 RESULT 9
 AAY70653
 ID AAY70653 standard; Protein; 202 AA.
 XX AAY70653;
 XX 18-JUL-2000 (first entry)
 XX Human transforming growth factor beta-9, ztgbeta-9 protein.
 XX Human transforming growth factor beta-9; ztgbeta-9;
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
 KW antiviral; cytostatic.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX Key 1..15
 FT Peptide /label= Signal_peptide
 FT

FT Protein 16..202
 /note= "Mature transforming growth factor beta-9"
 XX WO200015798-A2.
 XX 23-MAR-2000.
 XX 17-SEP-1999; 99WO-US21677.
 XX 17-SEP-1998; 98US-0154817.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Taft DW, Foley KP;
 XX WPI: 2000-271436/23.
 XX N-PSDB; AAZ52195.
 XX Polynucleotides encoding a novel transforming growth factor beta-9
 PT polypeptide, designated ztgb beta-9, useful as an antiviral and
 PT antiproliferative agent -
 XX Claim 6; Page 83; 97pp; English.
 CC The present sequence is the human transforming growth factor beta-9,
 CC designated ztgb beta-9. Human ztgb beta-9 was isolated from an arrayed
 CC pituitary gland cDNA plasmid library by PCR screening. This can be used
 CC to treat a variety of neurodegenerative diseases such as amyotrophic
 CC lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease,
 CC Parkinson's disease and peripheral neuropathies, or demyelinating
 CC diseases including multiple sclerosis. Ztgb beta-9 peptides have
 CC antiviral activity and may also be used to regulate the proliferation,
 CC differentiation and apoptosis of neurons, glial cells, lymphocytes,
 CC hematopoietic cells and stromal cells.
 XX Sequence 202 AA;
 SQ
 Query Match 100.0%; Score 729; DB 21; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.5e-74;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCPAGGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
 DB 70 scpaggrpadrrpptnlrsvspwayrissydparyprylpeayclrcgltlgfeadv 129
 QY 61 RFRSAPVYMTVVLRTPACAGRSVYTEAYVTIPVGCCTCPEPEKADBSINSSIDKQGA 120
 DB 130 rfrsapvymptvvlrrtpacagrsvyteayvtipvgctcpepekadsinsidkqga 189
 QY 121 KLLGPNDAAGP 133
 DB 190 killgpnadapagp 202
 RESULT 10
 AAY70662
 ID AAY70662 standard; Protein; 209 AA.
 XX AAY70662;
 XX 18-JUL-2000 (first entry)
 XX Human transforming growth factor beta-9, ztgbeta-9 variant protein.
 DE Human transforming growth factor beta-9; ztgbeta-9;
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
 KW antiviral; cytostatic.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX Key 1..15
 FT Peptide /label= Signal_peptide
 FT

QY 1 SCPAGGRADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
 Db 54 scpaggrpadrrfrpntnrsrswayrissydparyprylpeayclrcglcgtlfgfeedv 113
 QY 61 RFRSAPVYMPVTVLRTPACAGRSVYTYAYVTPVGCCTCVPEPEKADADSSIDKQGA 120
 Db 114 rfrsapvymptvvlrrtpacagrsvytyayvtipvgctcvpepekdadsinssidkqga 173
 QY 121 KLLGPNADAPAGP 133
 Db 174 kllgpnadapagp 186

RESULT 5
 AAY70654
 ID AAY70654 standard; Protein; 187 AA.
 XX
 AC AAY70654;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-1.
 XX
 KW Human transforming growth factor beta-9; Ztgfbeta-9;
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
 KW antiviral; cytosolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200015798-A2.
 XX
 PD 23-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US21677.
 XX
 PR 17-SEP-1998; 98US-0154817.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Taft DW, Foley KP;
 XX
 DR WPI; 2000-271436/23.
 DR N-PSDB; AA252195.
 XX
 PT Polynucleotides encoding a novel transforming growth factor beta-9
 PT polypeptide, designated Ztgfbeta-9, useful as an antiviral and
 PT antiproliferative agent
 XX
 PS Claim 6; Page 84; 97pp; English.
 XX
 CC The present sequence is the mature human transforming growth factor
 CC beta-9, designated Ztgfbeta-9. This is a mature sequence excluding the
 CC signal sequence extending from amino acid 16 to and including amino acid
 CC 202 of Ztgfbeta-9. Human Ztgfbeta-9 was isolated from an arrayed
 CC pituitary gland cDNA plasmid library by PCR screening. This can be used
 CC to treat a variety of neurodegenerative diseases such as amyotrophic
 CC lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease,
 CC Parkinson's disease and peripheral neuropathies, or demyelinating
 CC diseases including multiple sclerosis. Ztgfbeta-9 peptides have
 CC antiviral activity and may also be used to regulate the proliferation,
 CC differentiation and apoptosis of neurons, glial cells, lymphocytes,
 CC hematopoietic cells and stromal cells.
 XX
 SQ Sequence 187 AA;

Query Match 100.0%; Score 729; DB 21; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.4e-74;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
 Db 55 scpaggrpadrrfrpntnrsrswayrissydparyprylpeayclrcglcgtlfgfeedv 114
 QY 61 RFRSAPVYMPVTVLRTPACAGRSVYTYAYVTPVGCCTCVPEPEKADADSSIDKQGA 120
 Db 115 rfrsapvymptvvlrrtpacagrsvytyayvtipvgctcvpepekdadsinssidkqga 174
 QY 121 KLLGPNADAPAGP 133
 Db 175 kllgpnadapagp 187

RESULT 6
 AAY70663
 ID AAY70663 standard; Protein; 187 AA.
 XX
 AC AAY70663;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE Mature human Ztgfbeta-9 variant protein.
 XX
 KW Human transforming growth factor beta-9; Ztgfbeta-9;
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
 KW antiviral; cytosolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200015798-A2.
 XX
 PD 23-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US21677.
 XX
 PR 17-SEP-1998; 98US-0154817.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Taft DW, Foley KP;
 XX
 DR WPI; 2000-271436/23.
 DR N-PSDB; AA252201.
 XX
 PT Polynucleotides encoding a novel transforming growth factor beta-9
 PT polypeptide, designated Ztgfbeta-9, useful as an antiviral and
 PT antiproliferative agent
 XX
 PS Claim 6; Page 93-94; 97pp; English.
 XX
 CC The present sequence is a mature variant human transforming growth
 CC factor beta-9 protein, designated Ztgfbeta-9. Human Ztgfbeta-9 was
 CC isolated from an arrayed pituitary gland cDNA plasmid library by PCR
 CC screening. This can be used to treat a variety of neurodegenerative
 CC diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's
 CC disease, Huntington's disease, Parkinson's disease and peripheral
 CC neuropathies, or demyelinating diseases including multiple sclerosis.
 CC Ztgfbeta-9 peptides have antiviral activity and may also be used to
 CC regulate the proliferation, differentiation and apoptosis of neurons,
 CC glial cells, lymphocytes, hematopoietic cells and stromal cells.
 XX
 SQ Sequence 187 AA;

Query Match 100.0%; Score 729; DB 21; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.4e-74;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
 Db 55 scpaggrpadrrfrpntnrsrswayrissydparyprylpeayclrcglcgtlfgfeedv 114

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:19:50 ; Search time 21.13 Seconds
(without alignments)
381.590 Million cell updates/sec

Title: us-09-320-713-4_COPY_28_160

Perfect score: 729

Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLGPNAPAGP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 50623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
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3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	160	21	Partial amino acid
2	729	100.0	173	21	Partial amino acid
3	729	100.0	185	21	Mature human trans
4	729	100.0	186	21	Mature human trans
5	729	100.0	187	21	Mature human trans
6	729	100.0	187	21	Mature human trans
7	729	100.0	202	21	A human interleukin
8	729	100.0	202	21	A human interleukin
9	729	100.0	202	21	Human transforming
10	729	100.0	209	21	Human transforming
11	613	84.1	151	21	A human interleukin

12	613	84.1	151	21	AA807690	A rat interleukin-
13	601	82.4	183	21	AAV70658	Mature murine tran
14	601	82.4	205	21	AA807597	A murine interleuk
15	601	82.4	205	21	AA807691	A murine interleuk
16	601	82.4	205	21	AAV70657	Murine transformin
17	354	48.6	103	21	AA807688	A human interleuki
18	303	41.6	57	21	AAV70666	Human transforming
19	242	33.2	54	21	AAV70664	Human transforming
20	208	28.5	44	21	AA807596	A rat interleukin
21	193	26.5	425	21	AAV44462	Human interleukin
22	187.5	25.7	197	21	AA818911	A novel polypeptid
23	187.5	25.7	197	21	AA807602	A human interleuki
24	187.5	25.7	197	21	AA807684	A human interleuki
25	187.5	25.7	197	21	AAV92238	Human interleukin-
26	187.5	25.7	197	21	AAV44460	Human interleukin
27	187.5	25.7	197	21	AAV53892	Amino acid sequenc
28	187.5	25.7	206	21	AAV44485	Human interleukin
29	180	24.7	34	21	AAV70661	Human transforming
30	176.5	24.2	408	21	AAV44461	Human interleukin
31	174	23.9	128	21	AA85643	Human zcyto7 matur
32	174	23.9	130	21	AAV93975	Amino acid sequenc
33	174	23.9	151	20	AA85641	Human zcyto7 matur
34	174	23.9	153	20	AA85642	Human zcyto7 matur
35	174	23.9	154	20	AA85640	Human zcyto7 matur
36	174	23.9	157	20	AA85644	Human zcyto7 matur
37	174	23.9	158	20	AA85639	Human zcyto7 matur
38	174	23.9	160	20	AA85618	Human zcyto7 matur
39	174	23.9	160	20	AA85619	Human zcyto7 matur
40	174	23.9	160	20	AA85620	Human zcyto7 matur
41	174	23.9	160	20	AA85621	Human zcyto7 matur
42	174	23.9	160	20	AA85622	Human zcyto7 matur
43	174	23.9	160	20	AA85626	Human zcyto7 matur
44	174	23.9	160	20	AA85627	Human zcyto7 matur
45	174	23.9	160	20	AA85628	Human zcyto7 matur

ALIGNMENTS

RESULT 1

AAV53891
ID AAV53891 standard; Protein: 160 AA.

XX AC AAV53891;

XX AC AAV53891;

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